IM-5
SEQUENCE LISTING

<110> Wonderling, Ramani S.
Boroughs, Karen L.

<120> CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREOF

<130> IM-5

<140> not yet assigned
<141> 2001-07-27

<150> 60/223,016
<151> 2000-08-04

<160> 109

<170> PatentIn version 3.1

<210> 1
<211> 514
<212> DNA
<213> Felis catus

<220>
<221> CDS
<222> (114)..(512)
<223>

<220>
<221> misc_feature
<222> (470)..(470)
<223> n = unknown at position 470
Xaa = unknown at position 119

<400> 1
gctaaaggcg ctcctgccac cttctgccat ctacacagct caggaaaaga aagggacctc 60

aaaccttcca gatcccttcc tctcttagga aactattgag cacagggata aag atg 116
Met
1

act gct ata cca gta gat gat tgc atc aac ttt gtg gga atg aaa ttt 164
Thr Ala Ile Pro Val Asp Asp Cys Ile Asn Phe Val Gly Met Lys Phe
5 10 15

att gac aat aca ctt tac ttt gta gct gac agt gat gaa aac ctg gaa 212
Ile Asp Asn Thr Leu Tyr Phe Val Ala Asp Ser Asp Glu Asn Leu Glu
20 25 30

aca gat tac ttt ggc aag ctt gaa cat aaa ctc tca atc tta cga aac 260
Thr Asp Tyr Phe Gly Lys Leu Glu His Lys Leu Ser Ile Leu Arg Asn
35 40 45

ttg aac gac caa gtt ctc ttc att aac cag gga gat caa cct gtg ttt 308
Leu Asn Asp Gln Val Leu Phe Ile Asn Gln Gly Asp Gln Pro Val Phe
50 55 60 65

```
gag gat atg cct gat tct gac tgt aca gat aat gca ccc cgg act gaa      356
Glu Asp Met Pro Asp Ser Asp Cys Thr Asp Asn Ala Pro Arg Thr Glu
                70                  75                  80

ttt atc ata tat atg tat aaa gat agc ctc act aga ggt ctg gca gta      404
Phe Ile Ile Tyr Met Tyr Lys Asp Ser Leu Thr Arg Gly Leu Ala Val
            85                  90                  95

acc atc tct gtg aat tat aag acc atg tct act ctc tcc tgt gag aac      452
Thr Ile Ser Val Asn Tyr Lys Thr Met Ser Thr Leu Ser Cys Glu Asn
        100                 105                 110

aaa att att tcc ttt aan gga atg agt cct cct gag agt atc aat gat      500
Lys Ile Ile Ser Phe Xaa Gly Met Ser Pro Pro Glu Ser Ile Asn Asp
    115                 120                 125

gaa gga aat gac at                                                   514
Glu Gly Asn Asp
130
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<210> 2
<211> 133
<212> PRT
<213> Felis catus

<220>
<221> misc_feature
<222> (119)..(119)
<223> The 'Xaa' at location 119 stands for Lys, or Asn.

<220>
<221> misc_feature
<222> (470)..(470)
<223> n = unknown at position 470
Xaa = unknown at position 119

<400> 2

```
Met Thr Ala Ile Pro Val Asp Asp Cys Ile Asn Phe Val Gly Met Lys
1               5                   10                  15

Phe Ile Asp Asn Thr Leu Tyr Phe Val Ala Asp Ser Asp Glu Asn Leu
            20                  25                  30

Glu Thr Asp Tyr Phe Gly Lys Leu Glu His Lys Leu Ser Ile Leu Arg
        35                  40                  45

Asn Leu Asn Asp Gln Val Leu Phe Ile Asn Gln Gly Asp Gln Pro Val
    50                  55                  60

Phe Glu Asp Met Pro Asp Ser Asp Cys Thr Asp Asn Ala Pro Arg Thr
65                  70                  75                  80
```

Glu Phe Ile Ile Tyr Met Tyr Lys Asp Ser Leu Thr Arg Gly Leu Ala
85 90 95

Val Thr Ile Ser Val Asn Tyr Lys Thr Met Ser Thr Leu Ser Cys Glu
100 105 110

Asn Lys Ile Ile Ser Phe Xaa Gly Met Ser Pro Pro Glu Ser Ile Asn
115 120 125

Asp Glu Gly Asn Asp
130

<210> 3
<211> 514
<212> DNA
<213> Felis catus

<220>
<221> misc_feature
<222> (45)..(45)
<223> n = unknown at position 45

<400> 3
atgtcatttc cttcatcatt gatactctca ggaggactca ttccnttaaa ggaaataatt 60

ttgttctcac aggagagagt agacatggtc ttataattca cagagatggt tactgccaga 120

cctctagtga ggctatcttt atacatatat atgataaatt cagtccgggg tgcattatct 180

gtacagtcag aatcaggcat atcctcaaac acaggttgat ctccctggtt aatgaagaga 240

acttggtcgt tcaagtttcg taagattgag agtttatgtt caagcttgcc aaagtaatct 300

gtttccaggt tttcatcact gtcagctaca aagtaaagtg tattgtcaat aaatttcatt 360

cccacaaagt tgatgcaatc atctactggt atagcagtca tctttatccc tgtgctcaat 420

agtttcctaa gagaggaagg gatctggaag gtttgaggtc cctttctttt cctgagctgt 480

gtagatggca gaaggtggca ggagcgcctt tagc 514

<210> 4
<211> 502
<212> DNA
<213> Felis catus

<220>
<221> CDS
<222> (3)..(464)
<223>

<220>
<221> misc_feature
<222> (126)..(126)
<223> n = unknown at position 126
Xaa = unknown at position 43

<400> 4

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gc aag ctt gaa cat aaa ctc tca atc tta cga aac ttg aac gac caa        47
   Lys Leu Glu His Lys Leu Ser Ile Leu Arg Asn Leu Asn Asp Gln
   1               5                  10                  15

gtt ctc ttc att aac cag gga gat caa cct gtg ttt gag gat atg cct        95
Val Leu Phe Ile Asn Gln Gly Asp Gln Pro Val Phe Glu Asp Met Pro
                20                  25                  30

gat tct gac tgt aca gat aat gca ccc cgg nct gaa ttt atc ata tat       143
Asp Ser Asp Cys Thr Asp Asn Ala Pro Arg Xaa Glu Phe Ile Ile Tyr
            35                  40                  45

atg tat aaa gat agc ctc act aga ggt ctg gca gta acc atc tct gtg       191
Met Tyr Lys Asp Ser Leu Thr Arg Gly Leu Ala Val Thr Ile Ser Val
        50                  55                  60

aat tat aag acc atg tct act ctc tcc tgt gag aac aaa att att tcc       239
Asn Tyr Lys Thr Met Ser Thr Leu Ser Cys Glu Asn Lys Ile Ile Ser
    65                  70                  75

ttt aag gaa atg agt cct cct gag agt atc aat gat gaa gga aat gac       287
Phe Lys Glu Met Ser Pro Pro Glu Ser Ile Asn Asp Glu Gly Asn Asp
80                  85                  90                  95

atc ata ttc ttt cag aga agt gtt cca gga cat gat gat aag ata caa       335
Ile Ile Phe Phe Gln Arg Ser Val Pro Gly His Asp Asp Lys Ile Gln
                100                 105                 110

ttt gag tct tca ttg tac aag ggg tac ttt cta gct tgt gaa aaa gag       383
Phe Glu Ser Ser Leu Tyr Lys Gly Tyr Phe Leu Ala Cys Glu Lys Glu
            115                 120                 125

aaa gat ctt ttc aaa ctc att ttg aaa aaa aag gat gaa aat ggg gat       431
Lys Asp Leu Phe Lys Leu Ile Leu Lys Lys Lys Asp Glu Asn Gly Asp
        130                 135                 140

aag tcc ata atg ttc act gtt caa aac aag aat tagatattaa aattgcataa     484
Lys Ser Ile Met Phe Thr Val Gln Asn Lys Asn
    145                 150

tttgaaaaaa aaaaaaaa                                                  502
```

<210> 5
<211> 154
<212> PRT
<213> Felis catus

<220>
<221> misc_feature
<222> (42)..(42)

<223> The 'Xaa' at location 42 stands for Thr, Ala, Pro, or Ser.

<220>
<221> misc_feature
<222> (126)..(126)
<223> n = unknown at position 126
Xaa = unknown at position 43

<400> 5

```
Lys Leu Glu His Lys Leu Ser Ile Leu Arg Asn Leu Asn Asp Gln Val
1               5                  10                  15

Leu Phe Ile Asn Gln Gly Asp Gln Pro Val Phe Glu Asp Met Pro Asp
            20                  25                  30

Ser Asp Cys Thr Asp Asn Ala Pro Arg Xaa Glu Phe Ile Ile Tyr Met
        35                  40                  45

Tyr Lys Asp Ser Leu Thr Arg Gly Leu Ala Val Thr Ile Ser Val Asn
    50                  55                  60

Tyr Lys Thr Met Ser Thr Leu Ser Cys Glu Asn Lys Ile Ile Ser Phe
65                  70                  75                  80

Lys Glu Met Ser Pro Pro Glu Ser Ile Asn Asp Glu Gly Asn Asp Ile
                85                  90                  95

Ile Phe Phe Gln Arg Ser Val Pro Gly His Asp Asp Lys Ile Gln Phe
            100                 105                 110

Glu Ser Ser Leu Tyr Lys Gly Tyr Phe Leu Ala Cys Glu Lys Glu Lys
        115                 120                 125

Asp Leu Phe Lys Leu Ile Leu Lys Lys Lys Asp Glu Asn Gly Asp Lys
    130                 135                 140

Ser Ile Met Phe Thr Val Gln Asn Lys Asn
145                 150
```

<210> 6
<211> 502
<212> DNA
<213> Felis catus

<220>
<221> misc_feature
<222> (377)..(377)
<223> n = unknown at position 377

<400> 6
tttttttttt ttttcaaatt atgcaatttt aatatctaat tcttgttttg aacagtgaac 60

attatggact tatccccatt ttcatccttt tttttcaaaa tgagtttgaa aagatctttc 120

tctttttcac aagctagaaa gtacccccttg tacaatgaag actcaaattg tatcttatca 180

tcatgtcctg gaacacttct ctgaaagaat atgatgtcat ttccttcatc attgatactc 240

tcaggaggac tcatttcctt aaaggaaata attttgttct cacaggagag agtagacatg 300

gtcttataat tcacagagat ggttactgcc agacctctag tgaggctatc tttatacata 360

tatatgataa attcagnccg gggtgcatta tctgtacagt cagaatcagg catatcctca 420

aacacaggtt gatctccctg gttaatgaag agaacttggt cgttcaagtt tcgtaagatt 480

gagagtttat gttcaagctt gc 502

<210> 7
<211> 607
<212> DNA
<213> Felis catus

<220>
<221> CDS
<222> (24)..(599)
<223>

<400> 7
aactattgag cacagggata aag atg act gct ata cca gta gat gat tgc atc 53
Met Thr Ala Ile Pro Val Asp Asp Cys Ile
1 5 10

aac ttt gtg gga atg aaa ttt att gac aat aca ctt tac ttt gta gct 101
Asn Phe Val Gly Met Lys Phe Ile Asp Asn Thr Leu Tyr Phe Val Ala
15 20 25

gac agt gat gaa aac ctg gaa aca gat tac ttt ggc aag ctt gaa cat 149
Asp Ser Asp Glu Asn Leu Glu Thr Asp Tyr Phe Gly Lys Leu Glu His
30 35 40

aaa ctc tca atc tta cga aac ttg aac gac caa gtt ctc ttc att aac 197
Lys Leu Ser Ile Leu Arg Asn Leu Asn Asp Gln Val Leu Phe Ile Asn
45 50 55

cag gga gat caa cct gtg ttt gag gat atg cct gat tct gac tgt aca 245
Gln Gly Asp Gln Pro Val Phe Glu Asp Met Pro Asp Ser Asp Cys Thr
60 65 70

gat aat gca ccc cgg act gaa ttt atc ata tat atg tat aaa gat agc 293
Asp Asn Ala Pro Arg Thr Glu Phe Ile Ile Tyr Met Tyr Lys Asp Ser
75 80 85 90

ctc act aga ggt ctg gca gta acc atc tct gtg aat tat aag acc atg 341

```
Leu Thr Arg Gly Leu Ala Val Thr Ile Ser Val Asn Tyr Lys Thr Met
                95                  100                 105

tct act ctc tcc tgt gag aac aaa att att tcc ttt aag gaa atg agt      389
Ser Thr Leu Ser Cys Glu Asn Lys Ile Ile Ser Phe Lys Glu Met Ser
            110                 115                 120

cct cct gag agt atc aat gat gaa gga aat gac atc ata ttc ttt cag      437
Pro Pro Glu Ser Ile Asn Asp Glu Gly Asn Asp Ile Ile Phe Phe Gln
        125                 130                 135

aga agt gtt cca gga cat gat gat aag ata caa ttt gag tct tca ttg      485
Arg Ser Val Pro Gly His Asp Asp Lys Ile Gln Phe Glu Ser Ser Leu
    140                 145                 150

tac aag ggg tac ttt cta gct tgt gaa aaa gag aaa gat ctt ttc aaa      533
Tyr Lys Gly Tyr Phe Leu Ala Cys Glu Lys Glu Lys Asp Leu Phe Lys
155                 160                 165                 170

ctc att ttg aaa aaa aag gat gaa aat ggg gat aag tcc ata atg ttc      581
Leu Ile Leu Lys Lys Lys Asp Glu Asn Gly Asp Lys Ser Ile Met Phe
                175                 180                 185

act gtt caa aac aag aat tagatatt                                    607
Thr Val Gln Asn Lys Asn
            190
```

PCT/US2005/005

<210> 8
<211> 192
<212> PRT
<213> Felis catus

<400> 8

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Met Thr Ala Ile Pro Val Asp Asp Cys Ile Asn Phe Val Gly Met Lys
1               5                   10                  15

Phe Ile Asp Asn Thr Leu Tyr Phe Val Ala Asp Ser Asp Glu Asn Leu
            20                  25                  30

Glu Thr Asp Tyr Phe Gly Lys Leu Glu His Lys Leu Ser Ile Leu Arg
        35                  40                  45

Asn Leu Asn Asp Gln Val Leu Phe Ile Asn Gln Gly Asp Gln Pro Val
    50                  55                  60

Phe Glu Asp Met Pro Asp Ser Asp Cys Thr Asp Asn Ala Pro Arg Thr
65                  70                  75                  80

Glu Phe Ile Ile Tyr Met Tyr Lys Asp Ser Leu Thr Arg Gly Leu Ala
                85                  90                  95
```

Val Thr Ile Ser Val Asn Tyr Lys Thr Met Ser Thr Leu Ser Cys Glu
100 105 110

Asn Lys Ile Ile Ser Phe Lys Glu Met Ser Pro Pro Glu Ser Ile Asn
115 120 125

Asp Glu Gly Asn Asp Ile Ile Phe Phe Gln Arg Ser Val Pro Gly His
130 135 140

Asp Asp Lys Ile Gln Phe Glu Ser Ser Leu Tyr Lys Gly Tyr Phe Leu
145 150 155 160

Ala Cys Glu Lys Glu Lys Asp Leu Phe Lys Leu Ile Leu Lys Lys Lys
165 170 175

Asp Glu Asn Gly Asp Lys Ser Ile Met Phe Thr Val Gln Asn Lys Asn
180 185 190

<210> 9
<211> 576
<212> DNA
<213> Felis catus

<400> 9
atgactgcta taccagtaga tgattgcatc aactttgtgg gaatgaaatt tattgacaat 60

acactttact ttgtagctga cagtgatgaa aacctggaaa cagattactt tggcaagctt 120

gaacataaac tctcaatctt acgaaacttg aacgaccaag ttctcttcat taaccaggga 180

gatcaacctg tgtttgagga tatgcctgat tctgactgta cagataatgc accccggact 240

gaatttatca tatatatgta taaagatagc ctcactagag gtctggcagt aaccatctct 300

gtgaattata agaccatgtc tactctctcc tgtgagaaca aaattatttc ctttaaggaa 360

atgagtcctc ctgagagtat caatgatgaa ggaaatgaca tcatattctt tcagagaagt 420

gttccaggac atgatgataa gatacaattt gagtcttcat tgtacaaggg gtactttcta 480

gcttgtgaaa aagagaaaga tcttttcaaa ctcattttga aaaaaaagga tgaaaatggg 540

gataagtcca taatgttcac tgttcaaaac aagaat 576

<210> 10
<211> 607
<212> DNA
<213> Felis catus

<400> 10
aatatctaat tcttgttttg aacagtgaac attatggact tatccccatt ttcatccttt 60

```
tttttcaaaa tgagtttgaa aagatctttc tctttttcac aagctagaaa gtacccttg    120

tacaatgaag actcaaattg tatcttatca tcatgtcctg gaacacttct ctgaaagaat    180

atgatgtcat ttccttcatc attgatactc tcaggaggac tcatttcctt aaaggaaata    240

attttgttct cacaggagag agtagacatg gtcttataat tcacagagat ggttactgcc    300

agacctctag tgaggctatc tttatacata tatatgataa attcagtccg gggtgcatta    360

tctgtacagt cagaatcagg catatcctca aacacaggtt gatctccctg gttaatgaag    420

agaacttggt cgttcaagtt tcgtaagatt gagagtttat gttcaagctt gccaaagtaa    480

tctgtttcca ggttttcatc actgtcagct acaaagtaaa gtgtattgtc aataaatttc    540

attcccacaa agttgatgca atcatctact ggtatagcag tcatctttat ccctgtgctc    600

aatagtt                                                              607
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<210> 11
<211> 471
<212> DNA
<213> Felis catus

<220>
<221> CDS
<222> (1)..(471)
<223>

<400> 11

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tac ttt ggc aag ctt gaa cat aaa ctc tca atc tta cga aac ttg aac       48
Tyr Phe Gly Lys Leu Glu His Lys Leu Ser Ile Leu Arg Asn Leu Asn
1               5                  10                  15

gac caa gtt ctc ttc att aac cag gga gat caa cct gtg ttt gag gat       96
Asp Gln Val Leu Phe Ile Asn Gln Gly Asp Gln Pro Val Phe Glu Asp
            20                  25                  30

atg cct gat tct gac tgt aca gat aat gca ccc cgg act gaa ttt atc      144
Met Pro Asp Ser Asp Cys Thr Asp Asn Ala Pro Arg Thr Glu Phe Ile
        35                  40                  45

ata tat atg tat aaa gat agc ctc act aga ggt ctg gca gta acc atc      192
Ile Tyr Met Tyr Lys Asp Ser Leu Thr Arg Gly Leu Ala Val Thr Ile
    50                  55                  60

tct gtg aat tat aag acc atg tct act ctc tcc tgt gag aac aaa att      240
Ser Val Asn Tyr Lys Thr Met Ser Thr Leu Ser Cys Glu Asn Lys Ile
65                  70                  75                  80

att tcc ttt aag gaa atg agt cct cct gag agt atc aat gat gaa gga      288
Ile Ser Phe Lys Glu Met Ser Pro Pro Glu Ser Ile Asn Asp Glu Gly
                85                  90                  95

aat gac atc ata ttc ttt cag aga agt gtt cca gga cat gat gat aag      336
Asn Asp Ile Ile Phe Phe Gln Arg Ser Val Pro Gly His Asp Asp Lys
```

100 105 110

ata caa ttt gag tct tca ttg tac aag ggg tac ttt cta gct tgt gaa 384
Ile Gln Phe Glu Ser Ser Leu Tyr Lys Gly Tyr Phe Leu Ala Cys Glu
115 120 125

aaa gag aaa gat ctt ttc aaa ctc att ttg aaa aaa aag gat gaa aat 432
Lys Glu Lys Asp Leu Phe Lys Leu Ile Leu Lys Lys Lys Asp Glu Asn
130 135 140

ggg gat aag tcc ata atg ttc act gtt caa aac aag aat 471
Gly Asp Lys Ser Ile Met Phe Thr Val Gln Asn Lys Asn
145 150 155

<210> 12
<211> 157
<212> PRT
<213> Felis catus

<400> 12

Tyr Phe Gly Lys Leu Glu His Lys Leu Ser Ile Leu Arg Asn Leu Asn
1 5 10 15

Asp Gln Val Leu Phe Ile Asn Gln Gly Asp Gln Pro Val Phe Glu Asp
20 25 30

Met Pro Asp Ser Asp Cys Thr Asp Asn Ala Pro Arg Thr Glu Phe Ile
35 40 45

Ile Tyr Met Tyr Lys Asp Ser Leu Thr Arg Gly Leu Ala Val Thr Ile
50 55 60

Ser Val Asn Tyr Lys Thr Met Ser Thr Leu Ser Cys Glu Asn Lys Ile
65 70 75 80

Ile Ser Phe Lys Glu Met Ser Pro Pro Glu Ser Ile Asn Asp Glu Gly
85 90 95

Asn Asp Ile Ile Phe Phe Gln Arg Ser Val Pro Gly His Asp Asp Lys
100 105 110

Ile Gln Phe Glu Ser Ser Leu Tyr Lys Gly Tyr Phe Leu Ala Cys Glu
115 120 125

Lys Glu Lys Asp Leu Phe Lys Leu Ile Leu Lys Lys Lys Asp Glu Asn
130 135 140

Gly Asp Lys Ser Ile Met Phe Thr Val Gln Asn Lys Asn

145 150 155

<210> 13
<211> 471
<212> DNA
<213> Felis catus

<400> 13
attcttgttt tgaacagtga acattatgga cttatcccca ttttcatcct ttttttcaa 60

aatgagtttg aaaagatctt tctctttttc acaagctaga aagtacccct tgtacaatga 120

agactcaaat tgtatcttat catcatgtcc tggaacactt ctctgaaaga atatgatgtc 180

atttccttca tcattgatac tctcaggagg actcatttcc ttaaaggaaa taattttgtt 240

ctcacaggag agagtagaca tggtcttata attcacagag atggttactg ccagacctct 300

agtgaggcta tctttataca tatatatgat aaattcagtc cggggtgcat tatctgtaca 360

gtcagaatca ggcatatcct caaacacagg ttgatctccc tggttaatga agagaacttg 420

gtcgttcaag tttcgtaaga ttgagagttt atgttcaagc ttgccaaagt a 471

<210> 14
<211> 1233
<212> DNA
<213> Felis catus

<220>
<221> CDS
<222> (1)..(1230)
<223>

<400> 14
atg gcc gac aag gtc ctg aag gag aag agg aag cag ttc atc aac tca 48
Met Ala Asp Lys Val Leu Lys Glu Lys Arg Lys Gln Phe Ile Asn Ser
1 5 10 15

gtc ggc atg ggg acg gtc aac ggc ttg ctg gat gaa ctc ttt gag aaa 96
Val Gly Met Gly Thr Val Asn Gly Leu Leu Asp Glu Leu Phe Glu Lys
20 25 30

aac gtg ctg aac cag gag gag atg gag aga gta aaa tgt gaa aac gct 144
Asn Val Leu Asn Gln Glu Glu Met Glu Arg Val Lys Cys Glu Asn Ala
35 40 45

acc gtt atg gac aag gcc cga gct ctg atc gac agc gtc ctg cgg aaa 192
Thr Val Met Asp Lys Ala Arg Ala Leu Ile Asp Ser Val Leu Arg Lys
50 55 60

ggg cca cgg gcg tgc cag atc ttt atc tgt cac atc tgt gag gaa gac 240
Gly Pro Arg Ala Cys Gln Ile Phe Ile Cys His Ile Cys Glu Glu Asp
65 70 75 80

acc cac ctt gca gag acg ctg ggg ctc tcc tca agc cca caa tct gga 288

```
Thr His Leu Ala Glu Thr Leu Gly Leu Ser Ser Ser Pro Gln Ser Gly
                85                  90                  95

aat tct cag aac acc acg gac tct gaa gta gcg ttt cct cct ctt cca      336
Asn Ser Gln Asn Thr Thr Asp Ser Glu Val Ala Phe Pro Pro Leu Pro
            100                 105                 110

gcc agc gtg aat aac atg cct ggg ccg gct gag cca gaa gaa tct gta      384
Ala Ser Val Asn Asn Met Pro Gly Pro Ala Glu Pro Glu Glu Ser Val
        115                 120                 125

gat gct ctc aag ctt tgt cct cgt gaa aac ttc gtg aaa ctg tgt aaa      432
Asp Ala Leu Lys Leu Cys Pro Arg Glu Asn Phe Val Lys Leu Cys Lys
    130                 135                 140

cag agg gct gaa gag atc tac cca ata aag gag aga aag gat cgt act      480
Gln Arg Ala Glu Glu Ile Tyr Pro Ile Lys Glu Arg Lys Asp Arg Thr
145                 150                 155                 160

cgt ctg gct ctc atc ata tgc aat acg acg ttc gat cat ctt tct ctc      528
Arg Leu Ala Leu Ile Ile Cys Asn Thr Thr Phe Asp His Leu Ser Leu
                165                 170                 175

agg aag ggg gct gac ctt gac gtt gca ggg atg agg agg ctg ctt aca      576
Arg Lys Gly Ala Asp Leu Asp Val Ala Gly Met Arg Arg Leu Leu Thr
            180                 185                 190

gac ctt ggc tac agt gtg cac ata aaa gag gaa ctc act gct aag gac      624
Asp Leu Gly Tyr Ser Val His Ile Lys Glu Glu Leu Thr Ala Lys Asp
        195                 200                 205

atg gaa tca gag ctg agg gca ttt gct gcc cgt cca gag cac aag tcc      672
Met Glu Ser Glu Leu Arg Ala Phe Ala Ala Arg Pro Glu His Lys Ser
    210                 215                 220

tcg gac agc aca ttc ctg gtg ttc atg tct cat ggc atc ctg agt gga      720
Ser Asp Ser Thr Phe Leu Val Phe Met Ser His Gly Ile Leu Ser Gly
225                 230                 235                 240

atc tgt ggg acg aag tac agc gct gaa gga gac cca gat gta ttg gct      768
Ile Cys Gly Thr Lys Tyr Ser Ala Glu Gly Asp Pro Asp Val Leu Ala
                245                 250                 255

tat gac acc atc ttc cag att ttc aac aac cgc aac tgc ctt agt cta      816
Tyr Asp Thr Ile Phe Gln Ile Phe Asn Asn Arg Asn Cys Leu Ser Leu
            260                 265                 270

aag gac aag ccc aag gtc atc atc gtc cag gcc tgc aga ggt gaa aat      864
Lys Asp Lys Pro Lys Val Ile Ile Val Gln Ala Cys Arg Gly Glu Asn
        275                 280                 285

ttg ggg gaa ctg ttg atc agt gac tct cca gcg gcc cca atg gac agc      912
Leu Gly Glu Leu Leu Ile Ser Asp Ser Pro Ala Ala Pro Met Asp Ser
    290                 295                 300

act tca cag atg ggt agc agc ctt tca cag gtg ggt gac aac cta gag      960
Thr Ser Gln Met Gly Ser Ser Leu Ser Gln Val Gly Asp Asn Leu Glu
305                 310                 315                 320
```

```
gac gac gcc att tac aag gtc cac gtg gag aag gac ttc atc gct ttc     1008
Asp Asp Ala Ile Tyr Lys Val His Val Glu Lys Asp Phe Ile Ala Phe
                325                 330                 335

tgc tcc tcg acc cca cat cat gtg tct tgg aga gac gtg aac aag gga     1056
Cys Ser Ser Thr Pro His His Val Ser Trp Arg Asp Val Asn Lys Gly
            340                 345                 350

tct ctc ttc att aca caa ctc atc acg tgc ttc caa aag tat tcg tgg     1104
Ser Leu Phe Ile Thr Gln Leu Ile Thr Cys Phe Gln Lys Tyr Ser Trp
        355                 360                 365

tgc ttt cat ctg gag gaa gta ttt cgg aag gta caa cag tca ttt gaa     1152
Cys Phe His Leu Glu Glu Val Phe Arg Lys Val Gln Gln Ser Phe Glu
    370                 375                 380

aaa cca aat gtt aga gcc cag atg ccc acc att gaa cga cta tcc atg     1200
Lys Pro Asn Val Arg Ala Gln Met Pro Thr Ile Glu Arg Leu Ser Met
385                 390                 395                 400

aca aga tgt ttc tac ctc ttc cca gga cat taa                        1233
Thr Arg Cys Phe Tyr Leu Phe Pro Gly His
                405                 410
```

<210> 15
<211> 410
<212> PRT
<213> Felis catus

<400> 15

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Met Ala Asp Lys Val Leu Lys Glu Lys Arg Lys Gln Phe Ile Asn Ser
1               5                   10                  15

Val Gly Met Gly Thr Val Asn Gly Leu Leu Asp Glu Leu Phe Glu Lys
            20                  25                  30

Asn Val Leu Asn Gln Glu Glu Met Glu Arg Val Lys Cys Glu Asn Ala
        35                  40                  45

Thr Val Met Asp Lys Ala Arg Ala Leu Ile Asp Ser Val Leu Arg Lys
    50                  55                  60

Gly Pro Arg Ala Cys Gln Ile Phe Ile Cys His Ile Cys Glu Glu Asp
65                  70                  75                  80

Thr His Leu Ala Glu Thr Leu Gly Leu Ser Ser Ser Pro Gln Ser Gly
                85                  90                  95

Asn Ser Gln Asn Thr Thr Asp Ser Glu Val Ala Phe Pro Pro Leu Pro
            100                 105                 110
```

```
Ala Ser Val Asn Asn Met Pro Gly Pro Ala Glu Pro Glu Glu Ser Val
        115                 120                 125

Asp Ala Leu Lys Leu Cys Pro Arg Glu Asn Phe Val Lys Leu Cys Lys
    130                 135                 140

Gln Arg Ala Glu Glu Ile Tyr Pro Ile Lys Glu Arg Lys Asp Arg Thr
145                 150                 155                 160

Arg Leu Ala Leu Ile Ile Cys Asn Thr Thr Phe Asp His Leu Ser Leu
                165                 170                 175

Arg Lys Gly Ala Asp Leu Asp Val Ala Gly Met Arg Arg Leu Leu Thr
            180                 185                 190

Asp Leu Gly Tyr Ser Val His Ile Lys Glu Glu Leu Thr Ala Lys Asp
        195                 200                 205

Met Glu Ser Glu Leu Arg Ala Phe Ala Ala Arg Pro Glu His Lys Ser
    210                 215                 220

Ser Asp Ser Thr Phe Leu Val Phe Met Ser His Gly Ile Leu Ser Gly
225                 230                 235                 240

Ile Cys Gly Thr Lys Tyr Ser Ala Glu Gly Asp Pro Asp Val Leu Ala
                245                 250                 255

Tyr Asp Thr Ile Phe Gln Ile Phe Asn Asn Arg Asn Cys Leu Ser Leu
            260                 265                 270

Lys Asp Lys Pro Lys Val Ile Ile Val Gln Ala Cys Arg Gly Glu Asn
        275                 280                 285

Leu Gly Glu Leu Leu Ile Ser Asp Ser Pro Ala Ala Pro Met Asp Ser
    290                 295                 300

Thr Ser Gln Met Gly Ser Ser Leu Ser Gln Val Gly Asp Asn Leu Glu
305                 310                 315                 320

Asp Asp Ala Ile Tyr Lys Val His Val Glu Lys Asp Phe Ile Ala Phe
                325                 330                 335

Cys Ser Ser Thr Pro His His Val Ser Trp Arg Asp Val Asn Lys Gly
            340                 345                 350
```

Ser Leu Phe Ile Thr Gln Leu Ile Thr Cys Phe Gln Lys Tyr Ser Trp
355 360 365

Cys Phe His Leu Glu Glu Val Phe Arg Lys Val Gln Gln Ser Phe Glu
370 375 380

Lys Pro Asn Val Arg Ala Gln Met Pro Thr Ile Glu Arg Leu Ser Met
385 390 395 400

Thr Arg Cys Phe Tyr Leu Phe Pro Gly His
405 410

<210> 16
<211> 1233
<212> DNA
<213> Felis catus

<400> 16
ttaatgtcct gggaagaggt agaaacatct tgtcatggat agtcgttcaa tggtgggcat 60

ctgggctcta acatttggtt tttcaaatga ctgttgtacc ttccgaaata cttcctccag 120

atgaaagcac cacgaatact tttggaagca cgtgatgagt tgtgtaatga agagagatcc 180

cttgttcacg tctctccaag acacatgatg tggggtcgag gagcagaaag cgatgaagtc 240

cttctccacg tggaccttgt aaatggcgtc gtcctctagg ttgtcaccca cctgtgaaag 300

gctgctaccc atctgtgaag tgctgtccat tggggccgct ggagagtcac tgatcaacag 360

ttcccccaaa ttttcacctc tgcaggcctg gacgatgatg accttgggct tgtcctttag 420

actaaggcag ttgcggttgt tgaaaatctg gaagatggtg tcataagcca atacatctgg 480

gtctccttca gcgctgtact tcgtcccaca gattccactc aggatgccat gagacatgaa 540

caccaggaat gtgctgtccg aggacttgtg ctctggacgg gcagcaaatg ccctcagctc 600

tgattccatg tccttagcag tgagttcctc ttttatgtgc acactgtagc caaggtctgt 660

aagcagcctc ctcatccctg caacgtcaag gtcagccccc ttcctgagag aaagatgatc 720

gaacgtcgta ttgcatatga tgagagccag acgagtacga tccttttctct cctttattgg 780

gtagatctct tcagccctct gtttacacag tttcacgaag ttttcacgag gacaaagctt 840

gagagcatct acagattctt ctggctcagc cggcccaggc atgttattca cgctggctgg 900

aagaggagga aacgctactt cagagtccgt ggtgttctga gaatttccag attgtgggct 960

tgaggagagc cccagcgtct ctgcaaggtg ggtgtcttcc tcacagatgt gacagataaa 1020

gatctggcac gcccgtggcc ctttccgcag gacgctgtcg atcagagctc gggccttgtc 1080

cataacggta gcgttttcac attttactct ctccatctcc tcctggttca gcacgttttt 1140

ctcaaagagt tcatccagca agccgttgac cgtccccatg ccgactgagt tgatgaactg 1200

cttcctcttc tccttcagga ccttgtcggc cat 1233

<210> 17
<211> 526
<212> DNA
<213> Felis catus

<220>
<221> CDS
<222> (18)..(524)
<223>

<400> 17
ggcacgagca aaaagcc atg gcc gac aag gat ctg aag ggc aag agg aag 50
Met Ala Asp Lys Asp Leu Lys Gly Lys Arg Lys
1 5 10

cag ttc atc aac tca gtc ggc atg ggg acg gtc aac ggc ttg ctg gat 98
Gln Phe Ile Asn Ser Val Gly Met Gly Thr Val Asn Gly Leu Leu Asp
15 20 25

gaa ctc ttt gag aaa aac gtg ctg aac cag gag gag atg gag aga gta 146
Glu Leu Phe Glu Lys Asn Val Leu Asn Gln Glu Glu Met Glu Arg Val
30 35 40

aaa tgt gaa aac gct acc gtt atg gac aag gcc cga gct ctg atc gac 194
Lys Cys Glu Asn Ala Thr Val Met Asp Lys Ala Arg Ala Leu Ile Asp
45 50 55

agc gtc ctg cgg aaa ggg cca cgg gcg tgc cag atc ttt atc tgt cac 242
Ser Val Leu Arg Lys Gly Pro Arg Ala Cys Gln Ile Phe Ile Cys His
60 65 70 75

atc tgt gag gaa gac acc cac ctt gca gag acg ctg ggg ctc tcc tca 290
Ile Cys Glu Glu Asp Thr His Leu Ala Glu Thr Leu Gly Leu Ser Ser
80 85 90

agc cca caa tct gga aat tct cag aac acc acg gac tct gaa gta gcg 338
Ser Pro Gln Ser Gly Asn Ser Gln Asn Thr Thr Asp Ser Glu Val Ala
95 100 105

ttt cct cct ctt cca gcc agc gtg aat aac atg cct ggg ccg gct gag 386
Phe Pro Pro Leu Pro Ala Ser Val Asn Asn Met Pro Gly Pro Ala Glu
110 115 120

cca gaa gaa tct gta gat gct ctc aag ctt tgt cct cgt gaa aac ttc 434
Pro Glu Glu Ser Val Asp Ala Leu Lys Leu Cys Pro Arg Glu Asn Phe
125 130 135

gtg aaa ctg tgt aaa cag agg gct gaa gag atc tac cca ata aag gag 482
Val Lys Leu Cys Lys Gln Arg Ala Glu Glu Ile Tyr Pro Ile Lys Glu
140 145 150 155

```
aga aag gat cgt act cgt ctg gct ctc atc ata tgc aat acg ac          526
Arg Lys Asp Arg Thr Arg Leu Ala Leu Ile Ile Cys Asn Thr
                160                 165
```

<210> 18
<211> 169
<212> PRT
<213> Felis catus

<400> 18

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Met Ala Asp Lys Asp Leu Lys Gly Lys Arg Lys Gln Phe Ile Asn Ser
1               5                   10                  15

Val Gly Met Gly Thr Val Asn Gly Leu Leu Asp Glu Leu Phe Glu Lys
            20                  25                  30

Asn Val Leu Asn Gln Glu Glu Met Glu Arg Val Lys Cys Glu Asn Ala
        35                  40                  45

Thr Val Met Asp Lys Ala Arg Ala Leu Ile Asp Ser Val Leu Arg Lys
    50                  55                  60

Gly Pro Arg Ala Cys Gln Ile Phe Ile Cys His Ile Cys Glu Glu Asp
65                  70                  75                  80

Thr His Leu Ala Glu Thr Leu Gly Leu Ser Ser Ser Pro Gln Ser Gly
                85                  90                  95

Asn Ser Gln Asn Thr Thr Asp Ser Glu Val Ala Phe Pro Pro Leu Pro
            100                 105                 110

Ala Ser Val Asn Asn Met Pro Gly Pro Ala Glu Pro Glu Glu Ser Val
        115                 120                 125

Asp Ala Leu Lys Leu Cys Pro Arg Glu Asn Phe Val Lys Leu Cys Lys
    130                 135                 140

Gln Arg Ala Glu Glu Ile Tyr Pro Ile Lys Glu Arg Lys Asp Arg Thr
145                 150                 155                 160

Arg Leu Ala Leu Ile Ile Cys Asn Thr
                165
```

<210> 19
<211> 526

<212> DNA
<213> Felis catus

<400> 19
gtcgtattgc atatgatgag agccagacga gtacgatcct ttctctcctt tattgggtag 60

atctcttcag ccctctgttt acacagtttc acgaagtttt cacgaggaca aagcttgaga 120

gcatctacag attcttctgg ctcagccggc ccaggcatgt tattcacgct ggctggaaga 180

ggaggaaacg ctacttcaga gtccgtggtg ttctgagaat ttccagattg tgggcttgag 240

gagagcccca gcgtctctgc aaggtgggtg tcttcctcac agatgtgaca gataaagatc 300

tggcacgccc gtggcccttt ccgcaggacg ctgtcgatca gagctcgggc cttgtccata 360

acggtagcgt tttcacattt tactctctcc atctcctcct ggttcagcac gtttttctca 420

aagagttcat ccagcaagcc gttgaccgtc cccatgccga ctgagttgat gaactgcttc 480

ctcttgccct tcagatcctt gtcggccatg gctttttgct cgtgcc 526

<210> 20
<211> 500
<212> DNA
<213> Felis catus

<220>
<221> CDS
<222> (3)..(362)
<223>

<220>
<221> misc_feature
<222> (473)..(473)
<223> n = unknown at position 473

<400> 20
gg gaa ctg ttg atc agt gac tct cca gcg gcc cca atg gac agc act 47
Glu Leu Leu Ile Ser Asp Ser Pro Ala Ala Pro Met Asp Ser Thr
1 5 10 15

tca cag atg ggt agc agc ctt tca cag gtg ggt gac aac cta gag gac 95
Ser Gln Met Gly Ser Ser Leu Ser Gln Val Gly Asp Asn Leu Glu Asp
20 25 30

gac gcc att tac aag gtc cac gtg gag aag gac ttc atc gct ttc tgc 143
Asp Ala Ile Tyr Lys Val His Val Glu Lys Asp Phe Ile Ala Phe Cys
35 40 45

tcc tcg acc cca cat cat gtg tct tgg aga gac gtg aac aag gga tct 191
Ser Ser Thr Pro His His Val Ser Trp Arg Asp Val Asn Lys Gly Ser
50 55 60

ctc ttc att aca caa ctc atc acg tgc ttc caa aag tat tcg tgg tgc 239
Leu Phe Ile Thr Gln Leu Ile Thr Cys Phe Gln Lys Tyr Ser Trp Cys

65 70 75

ttt cat ctg gag gaa gta ttt cgg aag gta caa cag tca ttt gaa aaa 287
Phe His Leu Glu Glu Val Phe Arg Lys Val Gln Gln Ser Phe Glu Lys
80 85 90 95

cca aat gtt aga gcc cag atg ccc acc att gaa cga cta tcc atg aca 335
Pro Asn Val Arg Ala Gln Met Pro Thr Ile Glu Arg Leu Ser Met Thr
100 105 110

aga tac ttc tat ctc ttc cct ggc aat tgaaaatagc aatcatgggc 382
Arg Tyr Phe Tyr Leu Phe Pro Gly Asn
115 120

agtccagccc ttcttgacca acttggaaaa gtaccttagc tagcacaaca cactcattta 442

acgtttggta tctcaataaa aatgaaaaca nctaaaaaaa aaaaaaaaaa aaaaaaaa 500

<210> 21
<211> 120
<212> PRT
<213> Felis catus

<220>
<221> misc_feature
<222> (473)..(473)
<223> n = unknown at position 473

<400> 21

Glu Leu Leu Ile Ser Asp Ser Pro Ala Ala Pro Met Asp Ser Thr Ser
1 5 10 15

Gln Met Gly Ser Ser Leu Ser Gln Val Gly Asp Asn Leu Glu Asp Asp
20 25 30

Ala Ile Tyr Lys Val His Val Glu Lys Asp Phe Ile Ala Phe Cys Ser
35 40 45

Ser Thr Pro His His Val Ser Trp Arg Asp Val Asn Lys Gly Ser Leu
50 55 60

Phe Ile Thr Gln Leu Ile Thr Cys Phe Gln Lys Tyr Ser Trp Cys Phe
65 70 75 80

His Leu Glu Glu Val Phe Arg Lys Val Gln Gln Ser Phe Glu Lys Pro
85 90 95

Asn Val Arg Ala Gln Met Pro Thr Ile Glu Arg Leu Ser Met Thr Arg
100 105 110

Tyr Phe Tyr Leu Phe Pro Gly Asn
115 120

<210> 22
<211> 500
<212> DNA
<213> Felis catus

<220>
<221> misc_feature
<222> (28)..(28)
<223> n = unknown at position 28

<400> 22
tttttttttt tttttttttt tttttagntg ttttcatttt tattgagata ccaaacgtta 60

aatgagtgtg ttgtgctagc taaggtactt ttccaagttg gtcaagaagg gctggactgc 120

ccatgattgc tattttcaat tgccagggaa gagatagaag tatcttgtca tggatagtcg 180

ttcaatggtg ggcatctggg ctctaacatt tggtttttca aatgactgtt gtaccttccg 240

aaatacttcc tccagatgaa agcaccacga atacttttgg aagcacgtga tgagttgtgt 300

aatgaagaga gatcccttgt tcacgtctct ccaagacaca tgatgtgggg tcgaggagca 360

gaaagcgatg aagtccttct ccacgtggac cttgtaaatg gcgtcgtcct ctaggttgtc 420

acccacctgt gaaaggctgc tacccatctg tgaagtgctg tccattgggg ccgctggaga 480

gtcactgatc aacagttccc 500

<210> 23
<211> 1230
<212> DNA
<213> Felis catus

<220>
<221> CDS
<222> (1)..(1230)
<223>

<400> 23
atg gcc gac aag gat ctg aag ggc aag agg aag cag ttc atc aac tca 48
Met Ala Asp Lys Asp Leu Lys Gly Lys Arg Lys Gln Phe Ile Asn Ser
1 5 10 15

gtc ggc atg ggg acg gtc aac ggc ttg ctg gat gaa ctc ttt gag aaa 96
Val Gly Met Gly Thr Val Asn Gly Leu Leu Asp Glu Leu Phe Glu Lys
20 25 30

aac gtg ctg aac cag gag gag atg gag aga gta aaa tgt gaa aac gct 144
Asn Val Leu Asn Gln Glu Glu Met Glu Arg Val Lys Cys Glu Asn Ala
35 40 45

```
acc gtt atg gac aag gcc cga gct ctg atc gac agc gtc ctg cgg aaa      192
Thr Val Met Asp Lys Ala Arg Ala Leu Ile Asp Ser Val Leu Arg Lys
    50                  55                  60

ggg cca cgg gcg tgc cag atc ttt atc tgt cac atc tgt gag gaa gac      240
Gly Pro Arg Ala Cys Gln Ile Phe Ile Cys His Ile Cys Glu Glu Asp
65                  70                  75                  80

acc cac ctt gca gag acg ctg ggg ctc tcc tca agc cca caa tct gga      288
Thr His Leu Ala Glu Thr Leu Gly Leu Ser Ser Ser Pro Gln Ser Gly
                85                  90                  95

aat tct cag aac acc acg gac tct gaa gta gcg ttt cct cct ctt cca      336
Asn Ser Gln Asn Thr Thr Asp Ser Glu Val Ala Phe Pro Pro Leu Pro
            100                 105                 110

gcc agc gtg aat aac atg cct ggg ccg gct gag cca gaa gaa tct gta      384
Ala Ser Val Asn Asn Met Pro Gly Pro Ala Glu Pro Glu Glu Ser Val
        115                 120                 125

gat gct ctc aag ctt tgt cct cgt gaa aac ttc gtg aaa ctg tgt aaa      432
Asp Ala Leu Lys Leu Cys Pro Arg Glu Asn Phe Val Lys Leu Cys Lys
    130                 135                 140

cag agg gct gaa gag atc tac cca ata aag gag aga aag gat cgt act      480
Gln Arg Ala Glu Glu Ile Tyr Pro Ile Lys Glu Arg Lys Asp Arg Thr
145                 150                 155                 160

cgt ctg gct ctc atc ata tgc aat acg acg ttc gat cat ctt tct ctc      528
Arg Leu Ala Leu Ile Ile Cys Asn Thr Thr Phe Asp His Leu Ser Leu
                165                 170                 175

agg aag ggg gct gac ctt gac gtt gca ggg atg agg agg ctg ctt aca      576
Arg Lys Gly Ala Asp Leu Asp Val Ala Gly Met Arg Arg Leu Leu Thr
            180                 185                 190

gac ctt ggc tac agt gtg cac ata aaa gag gaa ctc act gct aag gac      624
Asp Leu Gly Tyr Ser Val His Ile Lys Glu Glu Leu Thr Ala Lys Asp
        195                 200                 205

atg gaa tca gag ctg agg gca ttt gct gcc cgt cca gag cac aag tcc      672
Met Glu Ser Glu Leu Arg Ala Phe Ala Ala Arg Pro Glu His Lys Ser
    210                 215                 220

tcg gac agc aca ttc ctg gtg ttc atg tct cat ggc atc ctg agt gga      720
Ser Asp Ser Thr Phe Leu Val Phe Met Ser His Gly Ile Leu Ser Gly
225                 230                 235                 240

atc tgt ggg acg aag tac agc gct gaa gga gac cca gat gta ttg gct      768
Ile Cys Gly Thr Lys Tyr Ser Ala Glu Gly Asp Pro Asp Val Leu Ala
                245                 250                 255

tat gac acc atc ttc cag att ttc aac aac cgc aac tgc ctt agt cta      816
Tyr Asp Thr Ile Phe Gln Ile Phe Asn Asn Arg Asn Cys Leu Ser Leu
            260                 265                 270

aag gac aag ccc aag gtc atc atc gtc cag gcc tgc aga ggt gaa aat      864
Lys Asp Lys Pro Lys Val Ile Ile Val Gln Ala Cys Arg Gly Glu Asn
        275                 280                 285
```

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ttg ggg gaa ctg ttg atc agt gac tct cca gcg gcc cca atg gac agc      912
Leu Gly Glu Leu Leu Ile Ser Asp Ser Pro Ala Ala Pro Met Asp Ser
    290                 295                 300

act tca cag atg ggt agc agc ctt tca cag gtg ggt gac aac cta gag      960
Thr Ser Gln Met Gly Ser Ser Leu Ser Gln Val Gly Asp Asn Leu Glu
305                 310                 315                 320

gac gac gcc att tac aag gtc cac gtg gag aag gac ttc atc gct ttc     1008
Asp Asp Ala Ile Tyr Lys Val His Val Glu Lys Asp Phe Ile Ala Phe
                325                 330                 335

tgc tcc tcg acc cca cat cat gtg tct tgg aga gac gtg aac aag gga     1056
Cys Ser Ser Thr Pro His His Val Ser Trp Arg Asp Val Asn Lys Gly
            340                 345                 350

tct ctc ttc att aca caa ctc atc acg tgc ttc caa aag tat tcg tgg     1104
Ser Leu Phe Ile Thr Gln Leu Ile Thr Cys Phe Gln Lys Tyr Ser Trp
        355                 360                 365

tgc ttt cat ctg gag gaa gta ttt cgg aag gta caa cag tca ttt gaa     1152
Cys Phe His Leu Glu Glu Val Phe Arg Lys Val Gln Gln Ser Phe Glu
    370                 375                 380

aaa cca aat gtt aga gcc cag atg ccc acc att gaa cga cta tcc atg     1200
Lys Pro Asn Val Arg Ala Gln Met Pro Thr Ile Glu Arg Leu Ser Met
385                 390                 395                 400

aca aga tac ttc tat ctc ttc cct ggc aat                            1230
Thr Arg Tyr Phe Tyr Leu Phe Pro Gly Asn
                405                 410
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<210> 24
<211> 410
<212> PRT
<213> Felis catus

<400> 24

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Met Ala Asp Lys Asp Leu Lys Gly Lys Arg Lys Gln Phe Ile Asn Ser
1               5                   10                  15

Val Gly Met Gly Thr Val Asn Gly Leu Leu Asp Glu Leu Phe Glu Lys
            20                  25                  30

Asn Val Leu Asn Gln Glu Glu Met Glu Arg Val Lys Cys Glu Asn Ala
        35                  40                  45

Thr Val Met Asp Lys Ala Arg Ala Leu Ile Asp Ser Val Leu Arg Lys
    50                  55                  60

Gly Pro Arg Ala Cys Gln Ile Phe Ile Cys His Ile Cys Glu Glu Asp
65                  70                  75                  80
```

Thr His Leu Ala Glu Thr Leu Gly Leu Ser Ser Ser Pro Gln Ser Gly
85 90 95

Asn Ser Gln Asn Thr Thr Asp Ser Glu Val Ala Phe Pro Pro Leu Pro
100 105 110

Ala Ser Val Asn Asn Met Pro Gly Pro Ala Glu Pro Glu Glu Ser Val
115 120 125

Asp Ala Leu Lys Leu Cys Pro Arg Glu Asn Phe Val Lys Leu Cys Lys
130 135 140

Gln Arg Ala Glu Glu Ile Tyr Pro Ile Lys Glu Arg Lys Asp Arg Thr
145 150 155 160

Arg Leu Ala Leu Ile Ile Cys Asn Thr Thr Phe Asp His Leu Ser Leu
165 170 175

Arg Lys Gly Ala Asp Leu Asp Val Ala Gly Met Arg Arg Leu Leu Thr
180 185 190

Asp Leu Gly Tyr Ser Val His Ile Lys Glu Glu Leu Thr Ala Lys Asp
195 200 205

Met Glu Ser Glu Leu Arg Ala Phe Ala Ala Arg Pro Glu His Lys Ser
210 215 220

Ser Asp Ser Thr Phe Leu Val Phe Met Ser His Gly Ile Leu Ser Gly
225 230 235 240

Ile Cys Gly Thr Lys Tyr Ser Ala Glu Gly Asp Pro Asp Val Leu Ala
245 250 255

Tyr Asp Thr Ile Phe Gln Ile Phe Asn Asn Arg Asn Cys Leu Ser Leu
260 265 270

Lys Asp Lys Pro Lys Val Ile Ile Val Gln Ala Cys Arg Gly Glu Asn
275 280 285

Leu Gly Glu Leu Leu Ile Ser Asp Ser Pro Ala Ala Pro Met Asp Ser
290 295 300

Thr Ser Gln Met Gly Ser Ser Leu Ser Gln Val Gly Asp Asn Leu Glu

305 310 315 320

Asp Asp Ala Ile Tyr Lys Val His Val Glu Lys Asp Phe Ile Ala Phe
325 330 335

Cys Ser Ser Thr Pro His His Val Ser Trp Arg Asp Val Asn Lys Gly
340 345 350

Ser Leu Phe Ile Thr Gln Leu Ile Thr Cys Phe Gln Lys Tyr Ser Trp
355 360 365

Cys Phe His Leu Glu Glu Val Phe Arg Lys Val Gln Gln Ser Phe Glu
370 375 380

Lys Pro Asn Val Arg Ala Gln Met Pro Thr Ile Glu Arg Leu Ser Met
385 390 395 400

Thr Arg Tyr Phe Tyr Leu Phe Pro Gly Asn
405 410

<210> 25
<211> 1230
<212> DNA
<213> Felis catus

<400> 25
attgccaggg aagagataga agtatcttgt catggatagt cgttcaatgg tgggcatctg 60

ggctctaaca tttggttttt caaatgactg ttgtaccttc cgaaatactt cctccagatg 120

aaagcaccac gaatactttt ggaagcacgt gatgagttgt gtaatgaaga gagatccctt 180

gttcacgtct ctccaagaca catgatgtgg ggtcgaggag cagaaagcga tgaagtcctt 240

ctccacgtgg accttgtaaa tggcgtcgtc ctctaggttg tcacccacct gtgaaaggct 300

gctacccatc tgtgaagtgc tgtccattgg ggccgctgga gagtcactga tcaacagttc 360

ccccaaattt tcacctctgc aggcctggac gatgatgacc ttgggcttgt cctttagact 420

aaggcagttg cggttgttga aaatctggaa gatggtgtca taagccaata catctgggtc 480

tccttcagcg ctgtacttcg tcccacagat tccactcagg atgccatgag acatgaacac 540

caggaatgtg ctgtccgagg acttgtgctc tggacgggca gcaaatgccc tcagctctga 600

ttccatgtcc ttagcagtga gttcctcttt tatgtgcaca ctgtagccaa ggtctgtaag 660

cagcctcctc atccctgcaa cgtcaaggtc agccccccttc ctgagagaaa gatgatcgaa 720

cgtcgtattg catatgatga gagccagacg agtacgatcc tttctctcct ttattgggta 780

gatctcttca gccctctgtt tacacagttt cacgaaggtt tcacgaggac aaagcttgag 840

agcatctaca gattcttctg gctcagccgg cccaggcatg ttattcacgc tggctggaag 900

aggaggaaac gctacttcag agtccgtggt gttctgagaa tttccagatt gtgggcttga 960

ggagagcccc agcgtctctg caaggtgggt gtcttcctca cagatgtgac agataaagat 1020

ctggcacgcc cgtggccctt tccgcaggac gctgtcgatc agagctcggg ccttgtccat 1080

aacggtagcg ttttcacatt ttactctctc catctcctcc tggttcagca cgtttttctc 1140

aaagagttca tccagcaagc cgttgaccgt ccccatgccg actgagttga tgaactgctt 1200

cctcttgccc ttcagatcct tgtcggccat 1230

<210> 26
<211> 921
<212> DNA
<213> Felis catus

<220>
<221> CDS
<222> (1)..(921)
<223>

<400> 26

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ata tgg gaa ctg gag aaa aac gtt tat gtt gta gag ttg gac tgg cac       48
Ile Trp Glu Leu Glu Lys Asn Val Tyr Val Val Glu Leu Asp Trp His
1               5                  10                  15

cct gat gcc ccc gga gaa atg gtg gtc ctc acc tgc aat act cct gaa       96
Pro Asp Ala Pro Gly Glu Met Val Val Leu Thr Cys Asn Thr Pro Glu
            20                  25                  30

gaa gat gac atc acc tgg acc tct gac cag agc agt gaa gtc cta ggc      144
Glu Asp Asp Ile Thr Trp Thr Ser Asp Gln Ser Ser Glu Val Leu Gly
        35                  40                  45

tct ggt aaa act ctg acc atc caa gtc aaa gaa ttt gca gat gct ggc      192
Ser Gly Lys Thr Leu Thr Ile Gln Val Lys Glu Phe Ala Asp Ala Gly
    50                  55                  60

cag tat acc tgt cat aaa gga ggc gag gtt ctg agc cat tcg ttc ctc      240
Gln Tyr Thr Cys His Lys Gly Gly Glu Val Leu Ser His Ser Phe Leu
65                  70                  75                  80

ctg ata cac aaa aag gaa gat gga att tgg tcc act gat atc tta agg      288
Leu Ile His Lys Lys Glu Asp Gly Ile Trp Ser Thr Asp Ile Leu Arg
                85                  90                  95

gaa cag aaa gaa tcc aaa aat aag atc ttt cta aaa tgt gag gca aag      336
Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe Leu Lys Cys Glu Ala Lys
            100                 105                 110

aat tat tct gga cgt ttc acc tgc tgg tgg ctg acg gca atc agt acc      384
Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp Leu Thr Ala Ile Ser Thr
```

```
        115                 120                 125

gat ttg aaa ttc act gtc aaa agc agc aga ggc tcc tct gac ccc caa      432
Asp Leu Lys Phe Thr Val Lys Ser Ser Arg Gly Ser Ser Asp Pro Gln
    130                 135                 140

gag gtg act tgt gga gca gcg aca ctc tca gca gag aag gtc aga gtg      480
Glu Val Thr Cys Gly Ala Ala Thr Leu Ser Ala Glu Lys Val Arg Val
145                 150                 155                 160

gac aac agg gat tat aag aag tac aca gtg gag tgt cag gag ggc agt      528
Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val Glu Cys Gln Glu Gly Ser
                165                 170                 175

gcc tgc ccg gct gcc gag gag agc cta ccc att gaa gtc gtg gtg gac      576
Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro Ile Glu Val Val Val Asp
            180                 185                 190

gct att cac aag ctc aag tac gaa aac tac acc agc agc ttc ttc atc      624
Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr Thr Ser Ser Phe Phe Ile
        195                 200                 205

agg gac atc atc aaa ccg gac cca ccc aag aac ctg caa ctg aag cca      672
Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys Asn Leu Gln Leu Lys Pro
    210                 215                 220

tta aaa aat tct cgg cat gtg gaa gtg agc tgg gaa tac cct gac acc      720
Leu Lys Asn Ser Arg His Val Glu Val Ser Trp Glu Tyr Pro Asp Thr
225                 230                 235                 240

tgg agc acc cca cat tcc tac ttc tcc tta aca ttt ggc gta cag gtc      768
Trp Ser Thr Pro His Ser Tyr Phe Ser Leu Thr Phe Gly Val Gln Val
                245                 250                 255

cag ggc aag aac aac aga gaa aag aaa gac aga ctc tcc gtg gac aag      816
Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp Arg Leu Ser Val Asp Lys
            260                 265                 270

acc tca gcc aag gtc gtg tgc cac aag gat gcc aag atc cgc gtg caa      864
Thr Ser Ala Lys Val Val Cys His Lys Asp Ala Lys Ile Arg Val Gln
        275                 280                 285

gcc aga gac cgc tac tat agc tca tcc tgg agc aac tgg gca tcc gtg      912
Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp Ser Asn Trp Ala Ser Val
    290                 295                 300

tcc tgc agt                                                         921
Ser Cys Ser
305
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<210> 27
<211> 307
<212> PRT
<213> Felis catus

<400> 27

Ile Trp Glu Leu Glu Lys Asn Val Tyr Val Val Glu Leu Asp Trp His

IM-5

```
1               5                   10                  15

Pro Asp Ala Pro Gly Glu Met Val Val Leu Thr Cys Asn Thr Pro Glu
            20                  25                  30

Glu Asp Asp Ile Thr Trp Thr Ser Asp Gln Ser Ser Glu Val Leu Gly
        35                  40                  45

Ser Gly Lys Thr Leu Thr Ile Gln Val Lys Glu Phe Ala Asp Ala Gly
    50                  55                  60

Gln Tyr Thr Cys His Lys Gly Gly Glu Val Leu Ser His Ser Phe Leu
65                  70                  75                  80

Leu Ile His Lys Lys Glu Asp Gly Ile Trp Ser Thr Asp Ile Leu Arg
                85                  90                  95

Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe Leu Lys Cys Glu Ala Lys
            100                 105                 110

Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp Leu Thr Ala Ile Ser Thr
        115                 120                 125

Asp Leu Lys Phe Thr Val Lys Ser Ser Arg Gly Ser Ser Asp Pro Gln
    130                 135                 140

Glu Val Thr Cys Gly Ala Ala Thr Leu Ser Ala Glu Lys Val Arg Val
145                 150                 155                 160

Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val Glu Cys Gln Glu Gly Ser
                165                 170                 175

Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro Ile Glu Val Val Val Asp
            180                 185                 190

Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr Thr Ser Ser Phe Phe Ile
        195                 200                 205

Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys Asn Leu Gln Leu Lys Pro
    210                 215                 220

Leu Lys Asn Ser Arg His Val Glu Val Ser Trp Glu Tyr Pro Asp Thr
225                 230                 235                 240
```

IM-5

Trp Ser Thr Pro His Ser Tyr Phe Ser Leu Thr Phe Gly Val Gln Val
245 250 255

Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp Arg Leu Ser Val Asp Lys
260 265 270

Thr Ser Ala Lys Val Val Cys His Lys Asp Ala Lys Ile Arg Val Gln
275 280 285

Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp Ser Asn Trp Ala Ser Val
290 295 300

Ser Cys Ser
305

<210> 28
<211> 921
<212> DNA
<213> Felis catus

<400> 28
actgcaggac acggatgccc agttgctcca ggatgagcta tagtagcggt ctctggcttg 60

cacgcggatc ttggcatcct tgtggcacac gaccttggct gaggtcttgt ccacggagag 120

tctgtctttc ttttctctgt tgttcttgcc ctggacctgt acgccaaatg ttaaggagaa 180

gtaggaatgt ggggtgctcc aggtgtcagg gtattcccag ctcacttcca catgccgaga 240

atttttaat ggcttcagtt gcaggttctt gggtgggtcc ggtttgatga tgtccctgat 300

gaagaagctg ctggtgtagt tttcgtactt gagcttgtga atagcgtcca ccacgacttc 360

aatgggtagg ctctcctcgg cagccgggca ggcactgccc tcctgacact ccactgtgta 420

cttcttataa tccctgttgt ccactctgac cttctctgct gagagtgtcg ctgctccaca 480

agtcacctct tgggggtcag aggagcctct gctgcttttg acagtgaatt tcaaatcggt 540

actgattgcc gtcagccacc agcaggtgaa acgtccagaa taattctttg cctcacattt 600

tagaaagatc ttatttttgg attctttctg ttcccttaag atatcagtgg accaaattcc 660

atcttccttt ttgtgtatca ggaggaacga atggctcaga acctcgcctc ctttatgaca 720

ggtatactgg ccagcatctg caaattcttt gacttggatg gtcagagttt taccagagcc 780

taggacttca ctgctctggt cagaggtcca ggtgatgtca tcttcttcag gagtattgca 840

ggtgaggacc accatttctc cgggggcatc agggtgccag tccaactcta caacataaac 900

gtttttctcc agttcccata t 921

<210> 29
<211> 987
<212> DNA
<213> Felis catus

<220>
<221> CDS
<222> (1)..(987)
<223>

<400> 29

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atg cat cct cag cag ttg gtc atc gcc tgg ttt tcc ctg gtt ttg ctg       48
Met His Pro Gln Gln Leu Val Ile Ala Trp Phe Ser Leu Val Leu Leu
1               5                   10                  15

gca cct ccc ctc atg gcc ata tgg gaa ctg gag aaa aac gtt tat gtt       96
Ala Pro Pro Leu Met Ala Ile Trp Glu Leu Glu Lys Asn Val Tyr Val
            20                  25                  30

gta gag ttg gac tgg cac cct gat gcc ccc gga gaa atg gtg gtc ctc      144
Val Glu Leu Asp Trp His Pro Asp Ala Pro Gly Glu Met Val Val Leu
        35                  40                  45

acc tgc aat act cct gaa gaa gat gac atc acc tgg acc tct gac cag      192
Thr Cys Asn Thr Pro Glu Glu Asp Asp Ile Thr Trp Thr Ser Asp Gln
    50                  55                  60

agc agt gaa gtc cta ggc tct ggt aaa act ctg acc atc caa gtc aaa      240
Ser Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys
65                  70                  75                  80

gaa ttt gca gat gct ggc cag tat acc tgt cat aaa gga ggc gag gtt      288
Glu Phe Ala Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Glu Val
                85                  90                  95

ctg agc cat tcg ttc ctc ctg ata cac aaa aag gaa gat gga att tgg      336
Leu Ser His Ser Phe Leu Leu Ile His Lys Lys Glu Asp Gly Ile Trp
            100                 105                 110

tcc act gat atc tta agg gaa cag aaa gaa tcc aaa aat aag atc ttt      384
Ser Thr Asp Ile Leu Arg Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe
        115                 120                 125

cta aaa tgt gag gca aag aat tat tct gga cgt ttc acc tgc tgg tgg      432
Leu Lys Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp
    130                 135                 140

ctg acg gca atc agt acc gat ttg aaa ttc act gtc aaa agc agc aga      480
Leu Thr Ala Ile Ser Thr Asp Leu Lys Phe Thr Val Lys Ser Ser Arg
145                 150                 155                 160

ggc tcc tct gac ccc caa ggg gtg act tgt gga gca gcg aca ctc tca      528
Gly Ser Ser Asp Pro Gln Gly Val Thr Cys Gly Ala Ala Thr Leu Ser
                165                 170                 175

gca gag aag gtc aga gtg gac aac agg gat tat aag aag tac aca gtg      576
Ala Glu Lys Val Arg Val Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val
            180                 185                 190
```

```
gag tgt cag gag ggc agt gcc tgc ccg gct gcc gag gag agc cta ccc      624
Glu Cys Gln Glu Gly Ser Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro
        195                 200                 205

att gaa gtc gtg gtg gac gct att cac aag ctc aag tac gaa aac tac      672
Ile Glu Val Val Val Asp Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr
    210                 215                 220

acc agc agc ttc ttc atc agg gac atc atc aaa ccg gac cca ccc aag      720
Thr Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys
225                 230                 235                 240

aac ctg caa ctg aag cca tta aaa aat tct cgg cat gtg gaa gtg agc      768
Asn Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg His Val Glu Val Ser
                245                 250                 255

tgg gaa tac cct gac acc tgg agc acc cca cat tcc tac ttc tcc tta      816
Trp Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu
            260                 265                 270

aca ttt ggc gta cag gtc cag ggc aag aac aac aga gaa aag aaa gac      864
Thr Phe Gly Val Gln Val Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp
        275                 280                 285

aga ctc tcc gtg gac aag acc tca gcc aag gtc gtg tgc cac aag gat      912
Arg Leu Ser Val Asp Lys Thr Ser Ala Lys Val Val Cys His Lys Asp
    290                 295                 300

gcc aag atc cgc gtg caa gcc aga gac cgc tac tat agc tca tcc tgg      960
Ala Lys Ile Arg Val Gln Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp
305                 310                 315                 320

agc aac tgg gca tcc gtg tcc tgc agt                                  987
Ser Asn Trp Ala Ser Val Ser Cys Ser
                325
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<210> 30
<211> 329
<212> PRT
<213> Felis catus

<400> 30

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Met His Pro Gln Gln Leu Val Ile Ala Trp Phe Ser Leu Val Leu Leu
1               5                   10                  15

Ala Pro Pro Leu Met Ala Ile Trp Glu Leu Glu Lys Asn Val Tyr Val
            20                  25                  30

Val Glu Leu Asp Trp His Pro Asp Ala Pro Gly Glu Met Val Val Leu
        35                  40                  45

Thr Cys Asn Thr Pro Glu Glu Asp Asp Ile Thr Trp Thr Ser Asp Gln
    50                  55                  60
```

Ser Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys
65 70 75 80

Glu Phe Ala Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Glu Val
85 90 95

Leu Ser His Ser Phe Leu Leu Ile His Lys Lys Glu Asp Gly Ile Trp
100 105 110

Ser Thr Asp Ile Leu Arg Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe
115 120 125

Leu Lys Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp
130 135 140

Leu Thr Ala Ile Ser Thr Asp Leu Lys Phe Thr Val Lys Ser Ser Arg
145 150 155 160

Gly Ser Ser Asp Pro Gln Gly Val Thr Cys Gly Ala Ala Thr Leu Ser
165 170 175

Ala Glu Lys Val Arg Val Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val
180 185 190

Glu Cys Gln Glu Gly Ser Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro
195 200 205

Ile Glu Val Val Val Asp Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr
210 215 220

Thr Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys
225 230 235 240

Asn Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg His Val Glu Val Ser
245 250 255

Trp Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu
260 265 270

Thr Phe Gly Val Gln Val Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp
275 280 285

Arg Leu Ser Val Asp Lys Thr Ser Ala Lys Val Val Cys His Lys Asp

290 295 300

Ala Lys Ile Arg Val Gln Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp
305 310 315 320

Ser Asn Trp Ala Ser Val Ser Cys Ser
325

<210> 31
<211> 987
<212> DNA
<213> Felis catus

<400> 31
actgcaggac acggatgccc agttgctcca ggatgagcta tagtagcggt ctctggcttg 60

cacgcggatc ttggcatcct tgtggcacac gaccttggct gaggtcttgt ccacggagag 120

tctgtctttc ttttctctgt tgttcttgcc ctggacctgt acgccaaatg ttaaggagaa 180

gtaggaatgt ggggtgctcc aggtgtcagg gtattcccag ctcacttcca catgccgaga 240

atttttaat ggcttcagtt gcaggttctt gggtgggtcc ggtttgatga tgtccctgat 300

gaagaagctg ctggtgtagt tttcgtactt gagcttgtga atagcgtcca ccacgacttc 360

aatgggtagg ctctcctcgg cagccgggca ggcactgccc tcctgacact ccactgtgta 420

cttcttataa tccctgttgt ccactctgac cttctctgct gagagtgtcg ctgctccaca 480

agtcacccct tgggggtcag aggagcctct gctgcttttg acagtgaatt tcaaatcggt 540

actgattgcc gtcagccacc agcaggtgaa acgtccagaa taattctttg cctcacattt 600

tagaaagatc ttatttttgg attctttctg ttcccttaag atatcagtgg accaaattcc 660

atcttccttt ttgtgtatca ggaggaacga atggctcaga acctcgcctc ctttatgaca 720

ggtatactgg ccagcatctg caaattcttt gacttggatg gtcagagttt taccagagcc 780

taggacttca ctgctctggt cagaggtcca ggtgatgtca tcttcttcag gagtattgca 840

ggtgaggacc accatttctc cgggggcatc agggtgccag tccaactcta caacataaac 900

gtttttctcc agttcccata tggccatgag gggaggtgcc agcaaaacca gggaaaacca 960

ggcgatgacc aactgctgag gatgcat 987

<210> 32
<211> 666
<212> DNA
<213> Felis catus

<220>
<221> CDS

<222> (1)..(666)
<223>

<400> 32

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atg tgc ccg ccg cgt ggc ctc ctc ctt gta acc atc ctg gtc ctg tta        48
Met Cys Pro Pro Arg Gly Leu Leu Leu Val Thr Ile Leu Val Leu Leu
1               5                   10                  15

aac cac ctg gac cac ctc agt ttg gcc agg aac ctc ccc aca ccc aca        96
Asn His Leu Asp His Leu Ser Leu Ala Arg Asn Leu Pro Thr Pro Thr
            20                  25                  30

cca agc cca gga atg ttc cag tgc ctc aac cac tcc caa acc ctg ctg       144
Pro Ser Pro Gly Met Phe Gln Cys Leu Asn His Ser Gln Thr Leu Leu
        35                  40                  45

cga gcc atc agc aac acg ctt cag aag gcc aga caa act cta gaa ttt       192
Arg Ala Ile Ser Asn Thr Leu Gln Lys Ala Arg Gln Thr Leu Glu Phe
    50                  55                  60

tac tcc tgc act tcc gaa gag att gat cat gaa gat atc aca aaa gat       240
Tyr Ser Cys Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys Asp
65                  70                  75                  80

aaa acc agc aca gtg gag gcc tgc tta cca ctg gaa tta acc atg aat       288
Lys Thr Ser Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Thr Met Asn
                85                  90                  95

gag agt tgc ctg gct tcc aga gag atc tct ctg ata act aat ggg agt       336
Glu Ser Cys Leu Ala Ser Arg Glu Ile Ser Leu Ile Thr Asn Gly Ser
            100                 105                 110

tgc ctg gcc tcc aga aag acc tct ttt atg acg acc ctg tgc ctt agc       384
Cys Leu Ala Ser Arg Lys Thr Ser Phe Met Thr Thr Leu Cys Leu Ser
        115                 120                 125

agt atc tat gag gac ttg aag atg tac cag gtg gag ttc aag gcc atg       432
Ser Ile Tyr Glu Asp Leu Lys Met Tyr Gln Val Glu Phe Lys Ala Met
    130                 135                 140

aat gca aag ctg tta atg gat cct aaa agg cag atc ttt ctg gat caa       480
Asn Ala Lys Leu Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp Gln
145                 150                 155                 160

aac atg ctg aca gct att gat gag ctg tta cag gcc ctg aat gtc aac       528
Asn Met Leu Thr Ala Ile Asp Glu Leu Leu Gln Ala Leu Asn Val Asn
                165                 170                 175

agt gtg act gtg cca cag aac tcc tcc ctg gaa gaa ccg gat ttt tat       576
Ser Val Thr Val Pro Gln Asn Ser Ser Leu Glu Glu Pro Asp Phe Tyr
            180                 185                 190

aaa act aaa atc aag ctc tgc ata ctt ctt cat gct ttc aga att cgt       624
Lys Thr Lys Ile Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile Arg
        195                 200                 205

gca gtg acc atc aat aga atg atg agc tat ctg aat gct tcc               666
Ala Val Thr Ile Asn Arg Met Met Ser Tyr Leu Asn Ala Ser
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210 215 220

<210> 33
<211> 222
<212> PRT
<213> Felis catus

<400> 33

Met Cys Pro Pro Arg Gly Leu Leu Leu Val Thr Ile Leu Val Leu Leu
1 5 10 15

Asn His Leu Asp His Leu Ser Leu Ala Arg Asn Leu Pro Thr Pro Thr
20 25 30

Pro Ser Pro Gly Met Phe Gln Cys Leu Asn His Ser Gln Thr Leu Leu
35 40 45

Arg Ala Ile Ser Asn Thr Leu Gln Lys Ala Arg Gln Thr Leu Glu Phe
50 55 60

Tyr Ser Cys Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys Asp
65 70 75 80

Lys Thr Ser Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Thr Met Asn
85 90 95

Glu Ser Cys Leu Ala Ser Arg Glu Ile Ser Leu Ile Thr Asn Gly Ser
100 105 110

Cys Leu Ala Ser Arg Lys Thr Ser Phe Met Thr Thr Leu Cys Leu Ser
115 120 125

Ser Ile Tyr Glu Asp Leu Lys Met Tyr Gln Val Glu Phe Lys Ala Met
130 135 140

Asn Ala Lys Leu Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp Gln
145 150 155 160

Asn Met Leu Thr Ala Ile Asp Glu Leu Leu Gln Ala Leu Asn Val Asn
165 170 175

Ser Val Thr Val Pro Gln Asn Ser Ser Leu Glu Glu Pro Asp Phe Tyr
180 185 190

Lys Thr Lys Ile Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile Arg

195 200 205

Ala Val Thr Ile Asn Arg Met Met Ser Tyr Leu Asn Ala Ser
210 215 220

<210> 34
<211> 666
<212> DNA
<213> Felis catus

<400> 34
ggaagcattc agatagctca tcattctatt gatggtcact gcacgaattc tgaaagcatg 60

aagaagtatg cagagcttga ttttagtttt ataaaaatcc ggttcttcca gggaggagtt 120

ctgtggcaca gtcacactgt tgacattcag ggcctgtaac agctcatcaa tagctgtcag 180

catgttttga tccagaaaga tctgcctttt aggatccatt aacagctttg cattcatggc 240

cttgaactcc acctggtaca tcttcaagtc ctcatagata ctgctaaggc acagggtcgt 300

cataaaagag gtctttctgg aggccaggca actcccatta gttatcagag agatctctct 360

ggaagccagg caactctcat tcatggttaa ttccagtggt aagcaggcct ccactgtgct 420

ggttttatct tttgtgatat cttcatgatc aatctcttcg gaagtgcagg agtaaaattc 480

tagagtttgt ctggccttct gaagcgtgtt gctgatggct cgcagcaggg tttgggagtg 540

gttgaggcac tggaacattc ctgggcttgg tgtgggtgtg gggaggttcc tggccaaact 600

gaggtggtcc aggtggttta acaggaccag gatggttaca aggaggaggc cacgcggcgg 660

gcacat 666

<210> 35
<211> 591
<212> DNA
<213> Felis catus

<220>
<221> CDS
<222> (1)..(591)
<223>

<400> 35
agg aac ctc ccc aca ccc aca cca agc cca gga atg ttc cag tgc ctc 48
Arg Asn Leu Pro Thr Pro Thr Pro Ser Pro Gly Met Phe Gln Cys Leu
1 5 10 15

aac cac tcc caa acc ctg ctg cga gcc atc agc aac acg ctt cag aag 96
Asn His Ser Gln Thr Leu Leu Arg Ala Ile Ser Asn Thr Leu Gln Lys
20 25 30

gcc aga caa act cta gaa ttt tac tcc tgc act tcc gaa gag att gat 144

```
Ala Arg Gln Thr Leu Glu Phe Tyr Ser Cys Thr Ser Glu Glu Ile Asp
        35                  40                  45

cat gaa gat atc aca aaa gat aaa acc agc aca gtg gag gcc tgc tta      192
His Glu Asp Ile Thr Lys Asp Lys Thr Ser Thr Val Glu Ala Cys Leu
    50                  55                  60

cca ctg gaa tta acc atg aat gag agt tgc ctg gct tcc aga gag atc      240
Pro Leu Glu Leu Thr Met Asn Glu Ser Cys Leu Ala Ser Arg Glu Ile
65                  70                  75                  80

tct ctg ata act aat ggg agt tgc ctg gcc tcc aga aag acc tct ttt      288
Ser Leu Ile Thr Asn Gly Ser Cys Leu Ala Ser Arg Lys Thr Ser Phe
                85                  90                  95

atg acg acc ctg tgc ctt agc agt atc tat gag gac ttg aag atg tac      336
Met Thr Thr Leu Cys Leu Ser Ser Ile Tyr Glu Asp Leu Lys Met Tyr
            100                 105                 110

cag gtg gag ttc aag gcc atg aat gca aag ctg tta atg gat cct aaa      384
Gln Val Glu Phe Lys Ala Met Asn Ala Lys Leu Leu Met Asp Pro Lys
        115                 120                 125

agg cag atc ttt ctg gat caa aac atg ctg aca gct att gat gag ctg      432
Arg Gln Ile Phe Leu Asp Gln Asn Met Leu Thr Ala Ile Asp Glu Leu
    130                 135                 140

tta cag gcc ctg aat gtc aac agt gtg act gtg cca cag aac tcc tcc      480
Leu Gln Ala Leu Asn Val Asn Ser Val Thr Val Pro Gln Asn Ser Ser
145                 150                 155                 160

ttg gaa gaa ccg gat ttt tat aaa act aaa atc aag ctc tgc ata ctt      528
Leu Glu Glu Pro Asp Phe Tyr Lys Thr Lys Ile Lys Leu Cys Ile Leu
                165                 170                 175

ctt cat gct ttc aga att cgt gca gtg acc atc aat aga atg atg agc      576
Leu His Ala Phe Arg Ile Arg Ala Val Thr Ile Asn Arg Met Met Ser
            180                 185                 190

tat ctg aat gct tcc                                                 591
Tyr Leu Asn Ala Ser
        195
```

<210> 36
<211> 197
<212> PRT
<213> Felis catus

<400> 36

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Arg Asn Leu Pro Thr Pro Thr Pro Ser Pro Gly Met Phe Gln Cys Leu
1               5                   10                  15

Asn His Ser Gln Thr Leu Leu Arg Ala Ile Ser Asn Thr Leu Gln Lys
            20                  25                  30
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Ala Arg Gln Thr Leu Glu Phe Tyr Ser Cys Thr Ser Glu Glu Ile Asp
35 40 45

His Glu Asp Ile Thr Lys Asp Lys Thr Ser Thr Val Glu Ala Cys Leu
50 55 60

Pro Leu Glu Leu Thr Met Asn Glu Ser Cys Leu Ala Ser Arg Glu Ile
65 70 75 80

Ser Leu Ile Thr Asn Gly Ser Cys Leu Ala Ser Arg Lys Thr Ser Phe
85 90 95

Met Thr Thr Leu Cys Leu Ser Ser Ile Tyr Glu Asp Leu Lys Met Tyr
100 105 110

Gln Val Glu Phe Lys Ala Met Asn Ala Lys Leu Leu Met Asp Pro Lys
115 120 125

Arg Gln Ile Phe Leu Asp Gln Asn Met Leu Thr Ala Ile Asp Glu Leu
130 135 140

Leu Gln Ala Leu Asn Val Asn Ser Val Thr Val Pro Gln Asn Ser Ser
145 150 155 160

Leu Glu Glu Pro Asp Phe Tyr Lys Thr Lys Ile Lys Leu Cys Ile Leu
165 170 175

Leu His Ala Phe Arg Ile Arg Ala Val Thr Ile Asn Arg Met Met Ser
180 185 190

Tyr Leu Asn Ala Ser
195

<210> 37
<211> 591
<212> DNA
<213> Felis catus

<400> 37
ggaagcattc agatagctca tcattctatt gatggtcact gcacgaattc tgaaagcatg 60

aagaagtatg cagagcttga ttttagtttt ataaaaatcc ggttcttcca aggaggagtt 120

ctgtggcaca gtcacactgt tgacattcag ggcctgtaac agctcatcaa tagctgtcag 180

catgttttga tccagaaaga tctgcctttt aggatccatt aacagctttg cattcatggc 240

cttgaactcc acctggtaca tcttcaagtc ctcatagata ctgctaaggc acagggtcgt 300

cataaaagag gtctttctgg aggccaggca actcccatta gttatcagag agatctctct 360

ggaagccagg caactctcat tcatggttaa ttccagtggt aagcaggcct ccactgtgct 420

ggttttatct tttgtgatat cttcatgatc aatctcttcg gaagtgcagg agtaaaattc 480

tagagtttgt ctggccttct gaagcgtgtt gctgatggct cgcagcaggg tttgggagtg 540

gttgaggcac tggaacattc ctgggcttgg tgtgggtgtg gggaggttcc t 591

<210> 38
<211> 1599
<212> DNA
<213> Felis catus

<220>
<221> CDS
<222> (1)..(1599)
<223>

<400> 38

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atg cat cct cag cag ttg gtc atc gcc tgg ctt tcc ctg gtt ttg ctg       48
Met His Pro Gln Gln Leu Val Ile Ala Trp Leu Ser Leu Val Leu Leu
1               5                   10                  15

gca cct ccc ctc atg gcc ata tgg gaa ctg gag aaa aac gtt tat gtt       96
Ala Pro Pro Leu Met Ala Ile Trp Glu Leu Glu Lys Asn Val Tyr Val
            20                  25                  30

gta gag ttg gac tgg cac cct gat gcc ccc gga gaa atg gtg gtc ctc      144
Val Glu Leu Asp Trp His Pro Asp Ala Pro Gly Glu Met Val Val Leu
        35                  40                  45

acc tgc aat act cct gaa gaa gat gac atc acc tgg acc tct gac cag      192
Thr Cys Asn Thr Pro Glu Glu Asp Asp Ile Thr Trp Thr Ser Asp Gln
    50                  55                  60

agc agt gaa gtc cta ggc tct ggt aaa act ctg acc atc caa gtc aaa      240
Ser Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys
65                  70                  75                  80

gaa ttt gca gat gct ggc cag tat acc tgt cat aaa gga ggc gag gtt      288
Glu Phe Ala Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Glu Val
                85                  90                  95

ctg agc cat tcg ttc ctc ctg ata cac aaa aag gaa gat gga att tgg      336
Leu Ser His Ser Phe Leu Leu Ile His Lys Lys Glu Asp Gly Ile Trp
            100                 105                 110

tcc act gat atc tta agg gaa cag aaa gaa tcc aaa aat aag atc ttt      384
Ser Thr Asp Ile Leu Arg Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe
        115                 120                 125

cta aaa tgt gag gca aag aat tat tct gga cgt ttc acc tgc tgg tgg      432
Leu Lys Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp
    130                 135                 140
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ctg acg gca atc agt acc gat ttg aaa ttc act gtc aaa agc agc aga      480
Leu Thr Ala Ile Ser Thr Asp Leu Lys Phe Thr Val Lys Ser Ser Arg
145                 150                 155                 160

ggc tcc tct gac ccc caa gag gtg act tgt gga gca gcg aca ctc tca      528
Gly Ser Ser Asp Pro Gln Glu Val Thr Cys Gly Ala Ala Thr Leu Ser
                165                 170                 175

gca gag aag gtc aga gtg gac aac agg gat tat aag aag tac aca gtg      576
Ala Glu Lys Val Arg Val Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val
            180                 185                 190

gag tgt cag gag ggc agt gcc tgc ccg gct gcc gag gag agc cta ccc      624
Glu Cys Gln Glu Gly Ser Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro
        195                 200                 205

att gaa gtc gtg gtg gac gct att cac aag ctc aag tac gaa aac tac      672
Ile Glu Val Val Val Asp Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr
    210                 215                 220

acc agc agc ttc ttc atc agg gac atc atc aaa ccg gac cca ccc aag      720
Thr Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys
225                 230                 235                 240

aac ctg caa ctg aag cca tta aaa aat tct cgg cat gtg gaa gtg agc      768
Asn Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg His Val Glu Val Ser
                245                 250                 255

tgg gaa tac cct gac acc tgg agc acc cca cat tcc tac ttc tcc tta      816
Trp Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu
            260                 265                 270

aca ttt ggc gta cag gtc cag ggc aag aac aac aga gaa aag aaa gac      864
Thr Phe Gly Val Gln Val Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp
        275                 280                 285

aga ctc tcc gtg gac aag acc tca gcc aag gtc gtg tgc cac aag gat      912
Arg Leu Ser Val Asp Lys Thr Ser Ala Lys Val Val Cys His Lys Asp
    290                 295                 300

gcc aag atc cgc gtg caa gcc aga gac cgc tac tat agc tca tcc tgg      960
Ala Lys Ile Arg Val Gln Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp
305                 310                 315                 320

agc aac tgg gca tcc gtg tcc tgc agt ggt ggc ggt ggc ggc gga tct     1008
Ser Asn Trp Ala Ser Val Ser Cys Ser Gly Gly Gly Gly Gly Gly Ser
                325                 330                 335

aga aac ttg cca acc cct act cca tcc ccg ggg atg ttc cag tgc ctc     1056
Arg Asn Leu Pro Thr Pro Thr Pro Ser Pro Gly Met Phe Gln Cys Leu
            340                 345                 350

aac cac tcc caa acc ctg ctg cga gcc atc agc aac acg ctt cag aag     1104
Asn His Ser Gln Thr Leu Leu Arg Ala Ile Ser Asn Thr Leu Gln Lys
        355                 360                 365

gcc aga caa act cta gaa ttt tac tcc tgc act tcc gaa gag att gat     1152
Ala Arg Gln Thr Leu Glu Phe Tyr Ser Cys Thr Ser Glu Glu Ile Asp
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    370                 375                 380

cat gaa gat atc aca aaa gat aaa acc agc aca gtg gag gcc tgc tta      1200
His Glu Asp Ile Thr Lys Asp Lys Thr Ser Thr Val Glu Ala Cys Leu
385                 390                 395                 400

cca ctg gaa tta acc atg aat gag agt tgc ctg gct tcc aga gag atc      1248
Pro Leu Glu Leu Thr Met Asn Glu Ser Cys Leu Ala Ser Arg Glu Ile
                405                 410                 415

tct ctg ata act aat ggg agt tgc ctg gcc tcc aga aag acc tct ttt      1296
Ser Leu Ile Thr Asn Gly Ser Cys Leu Ala Ser Arg Lys Thr Ser Phe
            420                 425                 430

atg acg acc ctg tgc ctt agc agt atc tat gag gac ttg aag atg tac      1344
Met Thr Thr Leu Cys Leu Ser Ser Ile Tyr Glu Asp Leu Lys Met Tyr
        435                 440                 445

cag gtg gag ttc aag gcc atg aat gca aag ctg tta atg gat cct aaa      1392
Gln Val Glu Phe Lys Ala Met Asn Ala Lys Leu Leu Met Asp Pro Lys
    450                 455                 460

agg cag atc ttt ctg gat caa aac atg ctg aca gct att gat gag ctg      1440
Arg Gln Ile Phe Leu Asp Gln Asn Met Leu Thr Ala Ile Asp Glu Leu
465                 470                 475                 480

tta cag gcc ctg aat gtc aac agt gtg act gtg cca cag aac tcc tcc      1488
Leu Gln Ala Leu Asn Val Asn Ser Val Thr Val Pro Gln Asn Ser Ser
                485                 490                 495

ttg gaa gaa ccg gat ttt tat aaa act aaa atc aag ctc tgc ata ctt      1536
Leu Glu Glu Pro Asp Phe Tyr Lys Thr Lys Ile Lys Leu Cys Ile Leu
            500                 505                 510

ctt cat gct ttc aga att cgt gca gtg acc atc aat aga atg atg agc      1584
Leu His Ala Phe Arg Ile Arg Ala Val Thr Ile Asn Arg Met Met Ser
        515                 520                 525

tat ctg aat gct tcc                                                 1599
Tyr Leu Asn Ala Ser
    530
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<210> 39
<211> 533
<212> PRT
<213> Felis catus

<400> 39

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Met His Pro Gln Gln Leu Val Ile Ala Trp Leu Ser Leu Val Leu Leu
1               5                   10                  15

Ala Pro Pro Leu Met Ala Ile Trp Glu Leu Glu Lys Asn Val Tyr Val
            20                  25                  30

Val Glu Leu Asp Trp His Pro Asp Ala Pro Gly Glu Met Val Val Leu
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35 40 45

Thr Cys Asn Thr Pro Glu Glu Asp Asp Ile Thr Trp Thr Ser Asp Gln
50 55 60

Ser Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys
65 70 75 80

Glu Phe Ala Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Glu Val
85 90 95

Leu Ser His Ser Phe Leu Leu Ile His Lys Lys Glu Asp Gly Ile Trp
100 105 110

Ser Thr Asp Ile Leu Arg Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe
115 120 125

Leu Lys Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp
130 135 140

Leu Thr Ala Ile Ser Thr Asp Leu Lys Phe Thr Val Lys Ser Ser Arg
145 150 155 160

Gly Ser Ser Asp Pro Gln Glu Val Thr Cys Gly Ala Ala Thr Leu Ser
165 170 175

Ala Glu Lys Val Arg Val Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val
180 185 190

Glu Cys Gln Glu Gly Ser Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro
195 200 205

Ile Glu Val Val Val Asp Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr
210 215 220

Thr Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys
225 230 235 240

Asn Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg His Val Glu Val Ser
245 250 255

Trp Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu
260 265 270

```
Thr Phe Gly Val Gln Val Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp
        275                 280                 285

Arg Leu Ser Val Asp Lys Thr Ser Ala Lys Val Val Cys His Lys Asp
    290                 295                 300

Ala Lys Ile Arg Val Gln Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp
305                 310                 315                 320

Ser Asn Trp Ala Ser Val Ser Cys Ser Gly Gly Gly Gly Gly Gly Ser
                325                 330                 335

Arg Asn Leu Pro Thr Pro Thr Pro Ser Pro Gly Met Phe Gln Cys Leu
            340                 345                 350

Asn His Ser Gln Thr Leu Leu Arg Ala Ile Ser Asn Thr Leu Gln Lys
        355                 360                 365

Ala Arg Gln Thr Leu Glu Phe Tyr Ser Cys Thr Ser Glu Glu Ile Asp
    370                 375                 380

His Glu Asp Ile Thr Lys Asp Lys Thr Ser Thr Val Glu Ala Cys Leu
385                 390                 395                 400

Pro Leu Glu Leu Thr Met Asn Glu Ser Cys Leu Ala Ser Arg Glu Ile
                405                 410                 415

Ser Leu Ile Thr Asn Gly Ser Cys Leu Ala Ser Arg Lys Thr Ser Phe
            420                 425                 430

Met Thr Thr Leu Cys Leu Ser Ser Ile Tyr Glu Asp Leu Lys Met Tyr
        435                 440                 445

Gln Val Glu Phe Lys Ala Met Asn Ala Lys Leu Leu Met Asp Pro Lys
    450                 455                 460

Arg Gln Ile Phe Leu Asp Gln Asn Met Leu Thr Ala Ile Asp Glu Leu
465                 470                 475                 480

Leu Gln Ala Leu Asn Val Asn Ser Val Thr Val Pro Gln Asn Ser Ser
                485                 490                 495

Leu Glu Glu Pro Asp Phe Tyr Lys Thr Lys Ile Lys Leu Cys Ile Leu
            500                 505                 510
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Leu His Ala Phe Arg Ile Arg Ala Val Thr Ile Asn Arg Met Met Ser
515 520 525

Tyr Leu Asn Ala Ser
530

<210> 40
<211> 1599
<212> DNA
<213> Felis catus

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aagaagtatg cagagcttga ttttagtttt ataaaaatcc ggttcttcca aggaggagtt 120

ctgtggcaca gtcacactgt tgacattcag ggcctgtaac agctcatcaa tagctgtcag 180

catgttttga tccagaaaga tctgcctttt aggatccatt aacagctttg cattcatggc 240

cttgaactcc acctggtaca tcttcaagtc ctcatagata ctgctaaggc acagggtcgt 300

cataaaagag gtctttctgg aggccaggca actcccatta gttatcagag agatctctct 360

ggaagccagg caactctcat tcatggttaa ttccagtggt aagcaggcct ccactgtgct 420

ggttttatct tttgtgatat cttcatgatc aatctcttcg gaagtgcagg agtaaaattc 480

tagagtttgt ctggccttct gaagcgtgtt gctgatggct cgcagcaggg tttgggagtg 540

gttgaggcac tggaacatcc ccggggatgg agtaggggtt ggcaagtttc tagatccgcc 600

gccaccgcca ccactgcagg acacggatgc ccagttgctc caggatgagc tatagtagcg 660

gtctctggct tgcacgcgga tcttggcatc cttgtggcac acgaccttgg ctgaggtctt 720

gtccacggag agtctgtctt tcttttctct gttgttcttg ccctggacct gtacgccaaa 780

tgttaaggag aagtaggaat gtggggtgct ccaggtgtca gggtattccc agctcacttc 840

cacatgccga gaatttttta atggcttcag ttgcaggttc ttgggtgggt ccggtttgat 900

gatgtccctg atgaagaagc tgctggtgta gttttcgtac ttgagcttgt gaatagcgtc 960

caccacgact tcaatgggta ggctctcctc ggcagccggg caggcactgc cctcctgaca 1020

ctccactgtg tacttcttat aatccctgtt gtccactctg accttctctg ctgagagtgt 1080

cgctgctcca caagtcacct cttgggggtc agaggagcct ctgctgcttt tgacagtgaa 1140

tttcaaatcg gtactgattg ccgtcagcca ccagcaggtg aaacgtccag aataattctt 1200

tgcctcacat tttagaaaga tcttattttt ggattctttc tgttccctta agatatcagt 1260

ggaccaaatt ccatcttcct ttttgtgtat caggaggaac gaatggctca gaacctcgcc 1320

tcctttatga caggtatact ggccagcatc tgcaaattct ttgacttgga tggtcagagt 1380

tttaccagag cctaggactt cactgctctg gtcagaggtc caggtgatgt catcttcttc 1440

aggagtattg caggtgagga ccaccatttc tccgggggca tcagggtgcc agtccaactc 1500

tacaacataa acgtttttct ccagttccca tatggccatg aggggaggtg ccagcaaaac 1560

cagggaaagc caggcgatga ccaactgctg aggatgcat 1599

<210> 41
<211> 576
<212> DNA
<213> Felis catus

<400> 41
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aaatgagttt gaaaagatct ttctcttttt cacaagctag aaagtacccc ttgtacaatg 120

aagactcaaa ttgtatctta tcatcatgtc ctggaacact tctctgaaag aatatgatgt 180

catttccttc atcattgata ctctcaggag gactcatttc cttaaaggaa ataattttgt 240

tctcacagga gagagtagac atggtcttat aattcacaga gatggttact gccagacctc 300

tagtgaggct atctttatac atatatatga taaattcagt ccggggtgca ttatctgtac 360

agtcagaatc aggcatatcc tcaaacacag gttgatctcc ctggttaatg aagagaactt 420

ggtcgttcaa gtttcgtaag attgagagtt tatgttcaag cttgccaaag taatctgttt 480

ccaggttttc atcactgtca gctacaaagt aaagtgtatt gtcaataaat ttcattccca 540

caaagttgat gcaatcatct actggtatag cagtca 576

<210> 42
<211> 0
<212> DNA
<213> Felis catus

<400> 42
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<210> 43
<211> 1533
<212> DNA
<213> Felis catus

<220>
<221> CDS
<222> (1)..(1533)
<223>

<400> 43
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IM-5

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Ile Trp Glu Leu Glu Lys Asn Val Tyr Val Val Glu Leu Asp Trp His
1               5                  10                  15

cct gat gcc ccc gga gaa atg gtg gtc ctc acc tgc aat act cct gaa      96
Pro Asp Ala Pro Gly Glu Met Val Val Leu Thr Cys Asn Thr Pro Glu
            20                  25                  30

gaa gat gac atc acc tgg acc tct gac cag agc agt gaa gtc cta ggc     144
Glu Asp Asp Ile Thr Trp Thr Ser Asp Gln Ser Ser Glu Val Leu Gly
        35                  40                  45

tct ggt aaa act ctg acc atc caa gtc aaa gaa ttt gca gat gct ggc     192
Ser Gly Lys Thr Leu Thr Ile Gln Val Lys Glu Phe Ala Asp Ala Gly
    50                  55                  60

cag tat acc tgt cat aaa gga ggc gag gtt ctg agc cat tcg ttc ctc     240
Gln Tyr Thr Cys His Lys Gly Gly Glu Val Leu Ser His Ser Phe Leu
65                  70                  75                  80

ctg ata cac aaa aag gaa gat gga att tgg tcc act gat atc tta agg     288
Leu Ile His Lys Lys Glu Asp Gly Ile Trp Ser Thr Asp Ile Leu Arg
                85                  90                  95

gaa cag aaa gaa tcc aaa aat aag atc ttt cta aaa tgt gag gca aag     336
Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe Leu Lys Cys Glu Ala Lys
            100                 105                 110

aat tat tct gga cgt ttc acc tgc tgg tgg ctg acg gca atc agt acc     384
Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp Leu Thr Ala Ile Ser Thr
        115                 120                 125

gat ttg aaa ttc act gtc aaa agc agc aga ggc tcc tct gac ccc caa     432
Asp Leu Lys Phe Thr Val Lys Ser Ser Arg Gly Ser Ser Asp Pro Gln
    130                 135                 140

gag gtg act tgt gga gca gcg aca ctc tca gca gag aag gtc aga gtg     480
Glu Val Thr Cys Gly Ala Ala Thr Leu Ser Ala Glu Lys Val Arg Val
145                 150                 155                 160

gac aac agg gat tat aag aag tac aca gtg gag tgt cag gag ggc agt     528
Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val Glu Cys Gln Glu Gly Ser
                165                 170                 175

gcc tgc ccg gct gcc gag gag agc cta ccc att gaa gtc gtg gtg gac     576
Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro Ile Glu Val Val Val Asp
            180                 185                 190

gct att cac aag ctc aag tac gaa aac tac acc agc agc ttc ttc atc     624
Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr Thr Ser Ser Phe Phe Ile
        195                 200                 205

agg gac atc atc aaa ccg gac cca ccc aag aac ctg caa ctg aag cca     672
Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys Asn Leu Gln Leu Lys Pro
    210                 215                 220

tta aaa aat tct cgg cat gtg gaa gtg agc tgg gaa tac cct gac acc     720
Leu Lys Asn Ser Arg His Val Glu Val Ser Trp Glu Tyr Pro Asp Thr
225                 230                 235                 240
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tgg agc acc cca cat tcc tac ttc tcc tta aca ttt ggc gta cag gtc      768
Trp Ser Thr Pro His Ser Tyr Phe Ser Leu Thr Phe Gly Val Gln Val
                245                 250                 255

cag ggc aag aac aac aga gaa aag aaa gac aga ctc tcc gtg gac aag      816
Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp Arg Leu Ser Val Asp Lys
            260                 265                 270

acc tca gcc aag gtc gtg tgc cac aag gat gcc aag atc cgc gtg caa      864
Thr Ser Ala Lys Val Val Cys His Lys Asp Ala Lys Ile Arg Val Gln
        275                 280                 285

gcc aga gac cgc tac tat agc tca tcc tgg agc aac tgg gca tcc gtg      912
Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp Ser Asn Trp Ala Ser Val
    290                 295                 300

tcc tgc agt ggt ggc ggt ggc ggc gga tct aga aac ttg cca acc cct      960
Ser Cys Ser Gly Gly Gly Gly Gly Gly Ser Arg Asn Leu Pro Thr Pro
305                 310                 315                 320

act cca tcc ccg ggg atg ttc cag tgc ctc aac cac tcc caa acc ctg     1008
Thr Pro Ser Pro Gly Met Phe Gln Cys Leu Asn His Ser Gln Thr Leu
                325                 330                 335

ctg cga gcc atc agc aac acg ctt cag aag gcc aga caa act cta gaa     1056
Leu Arg Ala Ile Ser Asn Thr Leu Gln Lys Ala Arg Gln Thr Leu Glu
            340                 345                 350

ttt tac tcc tgc act tcc gaa gag att gat cat gaa gat atc aca aaa     1104
Phe Tyr Ser Cys Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys
        355                 360                 365

gat aaa acc agc aca gtg gag gcc tgc tta cca ctg gaa tta acc atg     1152
Asp Lys Thr Ser Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Thr Met
    370                 375                 380

aat gag agt tgc ctg gct tcc aga gag atc tct ctg ata act aat ggg     1200
Asn Glu Ser Cys Leu Ala Ser Arg Glu Ile Ser Leu Ile Thr Asn Gly
385                 390                 395                 400

agt tgc ctg gcc tcc aga aag acc tct ttt atg acg acc ctg tgc ctt     1248
Ser Cys Leu Ala Ser Arg Lys Thr Ser Phe Met Thr Thr Leu Cys Leu
                405                 410                 415

agc agt atc tat gag gac ttg aag atg tac cag gtg gag ttc aag gcc     1296
Ser Ser Ile Tyr Glu Asp Leu Lys Met Tyr Gln Val Glu Phe Lys Ala
            420                 425                 430

atg aat gca aag ctg tta atg gat cct aaa agg cag atc ttt ctg gat     1344
Met Asn Ala Lys Leu Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp
        435                 440                 445

caa aac atg ctg aca gct att gat gag ctg tta cag gcc ctg aat gtc     1392
Gln Asn Met Leu Thr Ala Ile Asp Glu Leu Leu Gln Ala Leu Asn Val
    450                 455                 460

aac agt gtg act gtg cca cag aac tcc tcc ttg gaa gaa ccg gat ttt     1440
Asn Ser Val Thr Val Pro Gln Asn Ser Ser Leu Glu Glu Pro Asp Phe
465                 470                 475                 480
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tat aaa act aaa atc aag ctc tgc ata ctt ctt cat gct ttc aga att     1488
Tyr Lys Thr Lys Ile Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile
                485                 490                 495

cgt gca gtg acc atc aat aga atg atg agc tat ctg aat gct tcc         1533
Arg Ala Val Thr Ile Asn Arg Met Met Ser Tyr Leu Asn Ala Ser
            500                 505                 510
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<210> 44
<211> 511
<212> PRT
<213> Felis catus

<400> 44

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Ile Trp Glu Leu Glu Lys Asn Val Tyr Val Val Glu Leu Asp Trp His
1               5                   10                  15

Pro Asp Ala Pro Gly Glu Met Val Val Leu Thr Cys Asn Thr Pro Glu
            20                  25                  30

Glu Asp Asp Ile Thr Trp Thr Ser Asp Gln Ser Ser Glu Val Leu Gly
        35                  40                  45

Ser Gly Lys Thr Leu Thr Ile Gln Val Lys Glu Phe Ala Asp Ala Gly
    50                  55                  60

Gln Tyr Thr Cys His Lys Gly Gly Glu Val Leu Ser His Ser Phe Leu
65                  70                  75                  80

Leu Ile His Lys Lys Glu Asp Gly Ile Trp Ser Thr Asp Ile Leu Arg
                85                  90                  95

Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe Leu Lys Cys Glu Ala Lys
            100                 105                 110

Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp Leu Thr Ala Ile Ser Thr
        115                 120                 125

Asp Leu Lys Phe Thr Val Lys Ser Ser Arg Gly Ser Ser Asp Pro Gln
    130                 135                 140

Glu Val Thr Cys Gly Ala Ala Thr Leu Ser Ala Glu Lys Val Arg Val
145                 150                 155                 160

Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val Glu Cys Gln Glu Gly Ser
                165                 170                 175
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Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro Ile Glu Val Val Val Asp
180 185 190

Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr Thr Ser Ser Phe Phe Ile
195 200 205

Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys Asn Leu Gln Leu Lys Pro
210 215 220

Leu Lys Asn Ser Arg His Val Glu Val Ser Trp Glu Tyr Pro Asp Thr
225 230 235 240

Trp Ser Thr Pro His Ser Tyr Phe Ser Leu Thr Phe Gly Val Gln Val
245 250 255

Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp Arg Leu Ser Val Asp Lys
260 265 270

Thr Ser Ala Lys Val Val Cys His Lys Asp Ala Lys Ile Arg Val Gln
275 280 285

Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp Ser Asn Trp Ala Ser Val
290 295 300

Ser Cys Ser Gly Gly Gly Gly Gly Gly Ser Arg Asn Leu Pro Thr Pro
305 310 315 320

Thr Pro Ser Pro Gly Met Phe Gln Cys Leu Asn His Ser Gln Thr Leu
325 330 335

Leu Arg Ala Ile Ser Asn Thr Leu Gln Lys Ala Arg Gln Thr Leu Glu
340 345 350

Phe Tyr Ser Cys Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys
355 360 365

Asp Lys Thr Ser Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Thr Met
370 375 380

Asn Glu Ser Cys Leu Ala Ser Arg Glu Ile Ser Leu Ile Thr Asn Gly
385 390 395 400

Ser Cys Leu Ala Ser Arg Lys Thr Ser Phe Met Thr Thr Leu Cys Leu

405 410 415

Ser Ser Ile Tyr Glu Asp Leu Lys Met Tyr Gln Val Glu Phe Lys Ala
420 425 430

Met Asn Ala Lys Leu Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp
435 440 445

Gln Asn Met Leu Thr Ala Ile Asp Glu Leu Leu Gln Ala Leu Asn Val
450 455 460

Asn Ser Val Thr Val Pro Gln Asn Ser Ser Leu Glu Glu Pro Asp Phe
465 470 475 480

Tyr Lys Thr Lys Ile Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile
485 490 495

Arg Ala Val Thr Ile Asn Arg Met Met Ser Tyr Leu Asn Ala Ser
500 505 510

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<211> 1533
<212> DNA
<213> Felis catus

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aagaagtatg cagagcttga ttttagtttt ataaaaatcc ggttcttcca aggaggagtt 120

ctgtggcaca gtcacactgt tgacattcag ggcctgtaac agctcatcaa tagctgtcag 180

catgttttga tccagaaaga tctgcctttt aggatccatt aacagctttg cattcatggc 240

cttgaactcc acctggtaca tcttcaagtc ctcatagata ctgctaaggc acagggtcgt 300

cataaaagag gtctttctgg aggccaggca actcccatta gttatcagag agatctctct 360

ggaagccagg caactctcat tcatggttaa ttccagtggt aagcaggcct ccactgtgct 420

ggttttatct tttgtgatat cttcatgatc aatctcttcg gaagtgcagg agtaaaattc 480

tagagtttgt ctggccttct gaagcgtgtt gctgatggct cgcagcaggg tttgggagtg 540

gttgaggcac tggaacatcc ccggggatgg agtaggggtt ggcaagtttc tagatccgcc 600

gccaccgcca ccactgcagg acacggatgc ccagttgctc caggatgagc tatagtagcg 660

gtctctggct tgcacgcgga tcttggcatc cttgtggcac acgaccttgg ctgaggtctt 720

gtccacggag agtctgtctt tcttttctct gttgttcttg ccctggacct gtacgccaaa 780

tgttaaggag aagtaggaat gtggggtgct ccaggtgtca gggtattccc agctcacttc 840

cacatgccga gaatttttta atggcttcag ttgcaggttc ttgggtgggt ccggtttgat 900

gatgtccctg atgaagaagc tgctggtgta gttttcgtac ttgagcttgt gaatagcgtc 960

caccacgact tcaatgggta ggctctcctc ggcagccggg caggcactgc cctcctgaca 1020

ctccactgtg tacttcttat aatccctgtt gtccactctg accttctctg ctgagagtgt 1080

cgctgctcca caagtcacct cttgggggtc agaggagcct ctgctgcttt tgacagtgaa 1140

tttcaaatcg gtactgattg ccgtcagcca ccagcaggtg aaacgtccag aataattctt 1200

tgcctcacat tttagaaaga tcttattttt ggattctttc tgttccctta agatatcagt 1260

ggaccaaatt ccatcttcct ttttgtgtat caggaggaac gaatggctca gaacctcgcc 1320

tcctttatga caggtatact ggccagcatc tgcaaattct ttgacttgga tggtcagagt 1380

tttaccagag cctaggactt cactgctctg gtcagaggtc caggtgatgt catcttcttc 1440

aggagtattg caggtgagga ccaccatttc tccgggggca tcagggtgcc agtccaactc 1500

tacaacataa acgtttttct ccagttccca tat 1533

<210> 46
<211> 666
<212> DNA
<213> Canis familiaris

<220>
<221> CDS
<222> (1)..(666)
<223>

<400> 46

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atg tgc ccg ccg cgc ggc ctc ctc ctt gtg acc atc ctg gtc ctg cta       48
Met Cys Pro Pro Arg Gly Leu Leu Leu Val Thr Ile Leu Val Leu Leu
1               5                  10                  15

agc cac ctg gac cac ctt act tgg gcc agg agc ctc ccc aca gcc tca       96
Ser His Leu Asp His Leu Thr Trp Ala Arg Ser Leu Pro Thr Ala Ser
            20                  25                  30

ccg agc cca gga ata ttc cag tgc ctc aac cac tcc caa aac ctg ctg      144
Pro Ser Pro Gly Ile Phe Gln Cys Leu Asn His Ser Gln Asn Leu Leu
        35                  40                  45

aga gcc gtc agc aac acg ctt cag aag gcc aga caa act cta gaa tta      192
Arg Ala Val Ser Asn Thr Leu Gln Lys Ala Arg Gln Thr Leu Glu Leu
    50                  55                  60

tat tcc tgc act tcc gaa gag att gat cat gaa gat atc aca aag gat      240
Tyr Ser Cys Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys Asp
65                  70                  75                  80
```

```
aaa acc agc aca gtg gag gcc tgc tta cca ctg gaa tta acc atg aat      288
Lys Thr Ser Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Thr Met Asn
                85                  90                  95

gag agt tgc ctg gct tcc aga gag atc tct ttg ata act aac ggg agt      336
Glu Ser Cys Leu Ala Ser Arg Glu Ile Ser Leu Ile Thr Asn Gly Ser
            100                 105                 110

tgc ctg gcc tct gga aag gcc tct ttt atg acg gtc ctg tgc ctt agc      384
Cys Leu Ala Ser Gly Lys Ala Ser Phe Met Thr Val Leu Cys Leu Ser
        115                 120                 125

agc atc tat gag gac ttg aag atg tac cag atg gaa ttc aag gcc atg      432
Ser Ile Tyr Glu Asp Leu Lys Met Tyr Gln Met Glu Phe Lys Ala Met
    130                 135                 140

aac gca aag ctt tta atg gat ccc aag agg cag atc ttt ctg gat caa      480
Asn Ala Lys Leu Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp Gln
145                 150                 155                 160

aac atg ctg aca gct atc gat gag ctg tta cag gcc ctg aat ttc aac      528
Asn Met Leu Thr Ala Ile Asp Glu Leu Leu Gln Ala Leu Asn Phe Asn
                165                 170                 175

agt gtg act gtg cca cag aaa tcc tcc ctt gaa gag ccg gat ttt tat      576
Ser Val Thr Val Pro Gln Lys Ser Ser Leu Glu Glu Pro Asp Phe Tyr
            180                 185                 190

aaa act aaa atc aag ctc tgc ata ctt ctt cat gct ttc aga att cgt      624
Lys Thr Lys Ile Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile Arg
        195                 200                 205

gcg gtg acc atc gat aga atg atg agt tat ctg aat tct tcc              666
Ala Val Thr Ile Asp Arg Met Met Ser Tyr Leu Asn Ser Ser
    210                 215                 220
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<210> 47
<211> 222
<212> PRT
<213> Canis familiaris

<400> 47

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Met Cys Pro Pro Arg Gly Leu Leu Leu Val Thr Ile Leu Val Leu Leu
1               5                   10                  15

Ser His Leu Asp His Leu Thr Trp Ala Arg Ser Leu Pro Thr Ala Ser
            20                  25                  30

Pro Ser Pro Gly Ile Phe Gln Cys Leu Asn His Ser Gln Asn Leu Leu
        35                  40                  45

Arg Ala Val Ser Asn Thr Leu Gln Lys Ala Arg Gln Thr Leu Glu Leu
    50                  55                  60
```

Tyr Ser Cys Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys Asp
65 70 75 80

Lys Thr Ser Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Thr Met Asn
85 90 95

Glu Ser Cys Leu Ala Ser Arg Glu Ile Ser Leu Ile Thr Asn Gly Ser
100 105 110

Cys Leu Ala Ser Gly Lys Ala Ser Phe Met Thr Val Leu Cys Leu Ser
115 120 125

Ser Ile Tyr Glu Asp Leu Lys Met Tyr Gln Met Glu Phe Lys Ala Met
130 135 140

Asn Ala Lys Leu Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp Gln
145 150 155 160

Asn Met Leu Thr Ala Ile Asp Glu Leu Leu Gln Ala Leu Asn Phe Asn
165 170 175

Ser Val Thr Val Pro Gln Lys Ser Ser Leu Glu Glu Pro Asp Phe Tyr
180 185 190

Lys Thr Lys Ile Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile Arg
195 200 205

Ala Val Thr Ile Asp Arg Met Met Ser Tyr Leu Asn Ser Ser
210 215 220

<210> 48
<211> 666
<212> DNA
<213> Canis familiaris

<400> 48
ggaagaattc agataactca tcattctatc gatggtcacc gcacgaattc tgaaagcatg 60

aagaagtatg cagagcttga ttttagtttt ataaaaatcc ggctcttcaa gggaggattt 120

ctgtggcaca gtcacactgt tgaaattcag ggcctgtaac agctcatcga tagctgtcag 180

catgttttga tccagaaaga tctgcctctt gggatccatt aaaagctttg cgttcatggc 240

cttgaattcc atctggtaca tcttcaagtc ctcatagatg ctgctaaggc acaggaccgt 300

cataaaagag gcctttccag aggccaggca actcccgtta gttatcaaag agatctctct 360

ggaagccagg caactctcat tcatggttaa ttccagtggt aagcaggcct ccactgtgct 420

ggttttatcc tttgtgatat cttcatgatc aatctcttcg gaagtgcagg aatataattc 480

tagagtttgt ctggccttct gaagcgtgtt gctgacggct ctcagcaggt tttgggagtg 540

gttgaggcac tggaatattc ctgggctcgg tgaggctgtg gggaggctcc tggcccaagt 600

aaggtggtcc aggtggctta gcaggaccag gatggtcaca aggaggaggc cgcgcggcgg 660

gcacat 666

<210> 49
<211> 591
<212> DNA
<213> Canis familiaris

<220>
<221> CDS
<222> (1)..(591)
<223>

<400> 49

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agg agc ctc ccc aca gcc tca ccg agc cca gga ata ttc cag tgc ctc   48
Arg Ser Leu Pro Thr Ala Ser Pro Ser Pro Gly Ile Phe Gln Cys Leu
1               5                  10                  15

aac cac tcc caa aac ctg ctg aga gcc gtc agc aac acg ctt cag aag   96
Asn His Ser Gln Asn Leu Leu Arg Ala Val Ser Asn Thr Leu Gln Lys
            20                  25                  30

gcc aga caa act cta gaa tta tat tcc tgc act tcc gaa gag att gat  144
Ala Arg Gln Thr Leu Glu Leu Tyr Ser Cys Thr Ser Glu Glu Ile Asp
        35                  40                  45

cat gaa gat atc aca aag gat aaa acc agc aca gtg gag gcc tgc tta  192
His Glu Asp Ile Thr Lys Asp Lys Thr Ser Thr Val Glu Ala Cys Leu
    50                  55                  60

cca ctg gaa tta acc atg aat gag agt tgc ctg gct tcc aga gag atc  240
Pro Leu Glu Leu Thr Met Asn Glu Ser Cys Leu Ala Ser Arg Glu Ile
65                  70                  75                  80

tct ttg ata act aac ggg agt tgc ctg gcc tct gga aag gcc tct ttt  288
Ser Leu Ile Thr Asn Gly Ser Cys Leu Ala Ser Gly Lys Ala Ser Phe
                85                  90                  95

atg acg gtc ctg tgc ctt agc agc atc tat gag gac ttg aag atg tac  336
Met Thr Val Leu Cys Leu Ser Ser Ile Tyr Glu Asp Leu Lys Met Tyr
            100                 105                 110

cag atg gaa ttc aag gcc atg aac gca aag ctt tta atg gat ccc aag  384
Gln Met Glu Phe Lys Ala Met Asn Ala Lys Leu Leu Met Asp Pro Lys
        115                 120                 125

agg cag atc ttt ctg gat caa aac atg ctg aca gct atc gat gag ctg  432
Arg Gln Ile Phe Leu Asp Gln Asn Met Leu Thr Ala Ile Asp Glu Leu
```

130 135 140

tta cag gcc ctg aat ttc aac agt gtg act gtg cca cag aaa tcc tcc 480
Leu Gln Ala Leu Asn Phe Asn Ser Val Thr Val Pro Gln Lys Ser Ser
145 150 155 160

ctt gaa gag ccg gat ttt tat aaa act aaa atc aag ctc tgc ata ctt 528
Leu Glu Glu Pro Asp Phe Tyr Lys Thr Lys Ile Lys Leu Cys Ile Leu
165 170 175

ctt cat gct ttc aga att cgt gcg gtg acc atc gat aga atg atg agt 576
Leu His Ala Phe Arg Ile Arg Ala Val Thr Ile Asp Arg Met Met Ser
180 185 190

tat ctg aat tct tcc 591
Tyr Leu Asn Ser Ser
195

<210> 50
<211> 197
<212> PRT
<213> Canis familiaris

<400> 50

Arg Ser Leu Pro Thr Ala Ser Pro Ser Pro Gly Ile Phe Gln Cys Leu
1 5 10 15

Asn His Ser Gln Asn Leu Leu Arg Ala Val Ser Asn Thr Leu Gln Lys
20 25 30

Ala Arg Gln Thr Leu Glu Leu Tyr Ser Cys Thr Ser Glu Glu Ile Asp
35 40 45

His Glu Asp Ile Thr Lys Asp Lys Thr Ser Thr Val Glu Ala Cys Leu
50 55 60

Pro Leu Glu Leu Thr Met Asn Glu Ser Cys Leu Ala Ser Arg Glu Ile
65 70 75 80

Ser Leu Ile Thr Asn Gly Ser Cys Leu Ala Ser Gly Lys Ala Ser Phe
85 90 95

Met Thr Val Leu Cys Leu Ser Ser Ile Tyr Glu Asp Leu Lys Met Tyr
100 105 110

Gln Met Glu Phe Lys Ala Met Asn Ala Lys Leu Leu Met Asp Pro Lys
115 120 125

Arg Gln Ile Phe Leu Asp Gln Asn Met Leu Thr Ala Ile Asp Glu Leu

130 135 140

Leu Gln Ala Leu Asn Phe Asn Ser Val Thr Val Pro Gln Lys Ser Ser
145 150 155 160

Leu Glu Glu Pro Asp Phe Tyr Lys Thr Lys Ile Lys Leu Cys Ile Leu
165 170 175

Leu His Ala Phe Arg Ile Arg Ala Val Thr Ile Asp Arg Met Met Ser
180 185 190

Tyr Leu Asn Ser Ser
195

<210> 51
<211> 591
<212> DNA
<213> Canis familiaris

<400> 51
ggaagaattc agataactca tcattctatc gatggtcacc gcacgaattc tgaaagcatg 60

aagaagtatg cagagcttga ttttagtttt ataaaaatcc ggctcttcaa gggaggattt 120

ctgtggcaca gtcacactgt tgaaattcag ggcctgtaac agctcatcga tagctgtcag 180

catgttttga tccagaaaga tctgcctctt gggatccatt aaaagctttg cgttcatggc 240

cttgaattcc atctggtaca tcttcaagtc ctcatagatg ctgctaaggc acaggaccgt 300

cataaaagag gcctttccag aggccaggca actcccgtta gttatcaaag agatctctct 360

ggaagccagg caactctcat tcatggttaa ttccagtggt aagcaggcct ccactgtgct 420

ggttttatcc tttgtgatat cttcatgatc aatctcttcg gaagtgcagg aatataattc 480

tagagtttgt ctggccttct gaagcgtgtt gctgacggct ctcagcaggt tttgggagtg 540

gttgaggcac tggaatattc ctgggctcgg tgaggctgtg gggaggctcc t 591

<210> 52
<211> 921
<212> DNA
<213> Canis familiaris

<220>
<221> CDS
<222> (1)..(921)
<223>

<400> 52
ata tgg gaa ctg gag aaa gat gtt tat gtt gta gag ttg gac tgg cac 48

IM-5

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Ile Trp Glu Leu Glu Lys Asp Val Tyr Val Val Glu Leu Asp Trp His
1               5                  10                  15

cct gat gcc ccc gga gaa atg gtg gtc ctc acc tgc cat acc cct gaa  96
Pro Asp Ala Pro Gly Glu Met Val Val Leu Thr Cys His Thr Pro Glu
            20                  25                  30

gaa gat gac atc act tgg acc tca gcg cag agc agt gaa gtc cta ggt 144
Glu Asp Asp Ile Thr Trp Thr Ser Ala Gln Ser Ser Glu Val Leu Gly
        35                  40                  45

tct ggt aaa act ctg acc atc caa gtc aaa gaa ttt gga gat gct ggc 192
Ser Gly Lys Thr Leu Thr Ile Gln Val Lys Glu Phe Gly Asp Ala Gly
    50                  55                  60

cag tat acc tgc cat aaa gga ggc aag gtt ctg agc cgc tca ctc ctg 240
Gln Tyr Thr Cys His Lys Gly Gly Lys Val Leu Ser Arg Ser Leu Leu
65                  70                  75                  80

ttg att cac aaa aaa gaa gat gga att tgg tcc act gat atc tta aag 288
Leu Ile His Lys Lys Glu Asp Gly Ile Trp Ser Thr Asp Ile Leu Lys
                85                  90                  95

gaa cag aaa gaa tcc aaa aat aag atc ttt ctg aaa tgt gag gca aag 336
Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe Leu Lys Cys Glu Ala Lys
            100                 105                 110

aat tat tct gga cgt ttc aca tgc tgg tgg ctg acg gca atc agt act 384
Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp Leu Thr Ala Ile Ser Thr
        115                 120                 125

gat ttg aaa ttc agt gtc aaa agt agc aga ggc ttc tct gac ccc caa 432
Asp Leu Lys Phe Ser Val Lys Ser Ser Arg Gly Phe Ser Asp Pro Gln
    130                 135                 140

ggg gtg aca tgt gga gca gtg aca ctt tca gca gag agg gtc aga gtg 480
Gly Val Thr Cys Gly Ala Val Thr Leu Ser Ala Glu Arg Val Arg Val
145                 150                 155                 160

gac aac agg gat tat aag aag tac aca gtg gag tgt cag gag ggc agt 528
Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val Glu Cys Gln Glu Gly Ser
                165                 170                 175

gcc tgc ccc tct gcc gag gag agc cta ccc atc gag gtc gtg gtg gat 576
Ala Cys Pro Ser Ala Glu Glu Ser Leu Pro Ile Glu Val Val Val Asp
            180                 185                 190

gct att cac aag ctc aag tat gaa aac tac acc agc agc ttc ttc atc 624
Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr Thr Ser Ser Phe Phe Ile
        195                 200                 205

aga gac atc atc aaa cca gac cca ccc aca aac ctg cag ctg aag cca 672
Arg Asp Ile Ile Lys Pro Asp Pro Pro Thr Asn Leu Gln Leu Lys Pro
    210                 215                 220

ttg aaa aat tct cgg cac gtg gag gtc agc tgg gaa tac ccc gac acc 720
Leu Lys Asn Ser Arg His Val Glu Val Ser Trp Glu Tyr Pro Asp Thr
225                 230                 235                 240
```

```
tgg agc acc cca cat tcc tac ttc tcc ctg aca ttt tgc ata cag gcc      768
Trp Ser Thr Pro His Ser Tyr Phe Ser Leu Thr Phe Cys Ile Gln Ala
                245                 250                 255

cag ggc aag aac aat aga gaa aag aaa gat aga ctc tgc gtg gac aag      816
Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp Arg Leu Cys Val Asp Lys
            260                 265                 270

acc tca gcc aag gtc gtg tgc cac aag gat gcc aag atc cgc gtg caa      864
Thr Ser Ala Lys Val Val Cys His Lys Asp Ala Lys Ile Arg Val Gln
        275                 280                 285

gcc cga gac cgc tac tat agt tca tcc tgg agc gac tgg gca tct gtg      912
Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp Ser Asp Trp Ala Ser Val
    290                 295                 300

tcc tgc agt                                                         921
Ser Cys Ser
305
```

09/14/2005 15:09 FAX

<210> 53
<211> 307
<212> PRT
<213> Canis familiaris

<400> 53

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Ile Trp Glu Leu Glu Lys Asp Val Tyr Val Val Glu Leu Asp Trp His
1               5                   10                  15

Pro Asp Ala Pro Gly Glu Met Val Val Leu Thr Cys His Thr Pro Glu
            20                  25                  30

Glu Asp Asp Ile Thr Trp Thr Ser Ala Gln Ser Ser Glu Val Leu Gly
        35                  40                  45

Ser Gly Lys Thr Leu Thr Ile Gln Val Lys Glu Phe Gly Asp Ala Gly
    50                  55                  60

Gln Tyr Thr Cys His Lys Gly Gly Lys Val Leu Ser Arg Ser Leu Leu
65                  70                  75                  80

Leu Ile His Lys Lys Glu Asp Gly Ile Trp Ser Thr Asp Ile Leu Lys
                85                  90                  95

Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe Leu Lys Cys Glu Ala Lys
            100                 105                 110

Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp Leu Thr Ala Ile Ser Thr
        115                 120                 125
```

Asp Leu Lys Phe Ser Val Lys Ser Ser Arg Gly Phe Ser Asp Pro Gln
130 135 140

Gly Val Thr Cys Gly Ala Val Thr Leu Ser Ala Glu Arg Val Arg Val
145 150 155 160

Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val Glu Cys Gln Glu Gly Ser
165 170 175

Ala Cys Pro Ser Ala Glu Glu Ser Leu Pro Ile Glu Val Val Val Asp
180 185 190

Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr Thr Ser Ser Phe Phe Ile
195 200 205

Arg Asp Ile Ile Lys Pro Asp Pro Pro Thr Asn Leu Gln Leu Lys Pro
210 215 220

Leu Lys Asn Ser Arg His Val Glu Val Ser Trp Glu Tyr Pro Asp Thr
225 230 235 240

Trp Ser Thr Pro His Ser Tyr Phe Ser Leu Thr Phe Cys Ile Gln Ala
245 250 255

Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp Arg Leu Cys Val Asp Lys
260 265 270

Thr Ser Ala Lys Val Val Cys His Lys Asp Ala Lys Ile Arg Val Gln
275 280 285

Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp Ser Asp Trp Ala Ser Val
290 295 300

Ser Cys Ser
305

<210> 54
<211> 921
<212> DNA
<213> Canis familiaris

<400> 54
actgcaggac acagatgccc agtcgctcca ggatgaacta tagtagcggt ctcgggcttg 60

cacgcggatc ttggcatcct tgtggcacac gaccttggct gaggtcttgt ccacgcagag 120

tctatctttc ttttctctat tgttcttgcc ctgggcctgt atgcaaaatg tcagggagaa 180

gtaggaatgt ggggtgctcc aggtgtcggg gtattcccag ctgacctcca cgtgccgaga 240

atttttcaat ggcttcagct gcaggtttgt gggtgggtct ggtttgatga tgtctctgat 300

gaagaagctg ctggtgtagt tttcatactt gagcttgtga atagcatcca ccacgacctc 360

gatgggtagg ctctcctcgg cagaggggca ggcactgccc tcctgacact ccactgtgta 420

cttcttataa tccctgttgt ccactctgac cctctctgct gaaagtgtca ctgctccaca 480

tgtcacccct tgggggtcag agaagcctct gctacttttg acactgaatt tcaaatcagt 540

actgattgcc gtcagccacc agcatgtgaa acgtccagaa taattctttg cctcacattt 600

cagaaagatc ttatttttgg attctttctg ttcctttaag atatcagtgg accaaattcc 660

atcttctttt ttgtgaatca acaggagtga gcggctcaga accttgcctc ctttatggca 720

ggtatactgg ccagcatctc caaattcttt gacttggatg gtcagagttt taccagaacc 780

taggacttca ctgctctgcg ctgaggtcca agtgatgtca tcttcttcag gggtatggca 840

ggtgaggacc accatttctc cgggggcatc agggtgccag tccaactcta caacataaac 900

atctttctcc agttcccata t 921

<210> 55
<211> 985
<212> DNA
<213> Felis catus

<220>
<221> CDS
<222> (1)..(984)
<223>

<400> 55

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atg cat cct cag cag ttg gtc atc gcc tgg ttt tcc ctg gtt ttg ctg       48
Met His Pro Gln Gln Leu Val Ile Ala Trp Phe Ser Leu Val Leu Leu
1               5                  10                  15

gca cct ccc ctc atg gcc ata tgg gaa ctg gag aaa aac gtt tat gtt       96
Ala Pro Pro Leu Met Ala Ile Trp Glu Leu Glu Lys Asn Val Tyr Val
            20                  25                  30

gta gag ttg gac tgg cac cct gat gcc ccc gga gaa atg gtg gtc ctc      144
Val Glu Leu Asp Trp His Pro Asp Ala Pro Gly Glu Met Val Val Leu
        35                  40                  45

acc tgc aat act cct gaa gaa gat gac atc acc tgg acc tct gac cag      192
Thr Cys Asn Thr Pro Glu Glu Asp Asp Ile Thr Trp Thr Ser Asp Gln
    50                  55                  60

agc agt gaa gtc cta ggc tct ggt aaa act ctg acc atc caa gtc aaa      240
Ser Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys
```

```
65                  70                  75                  80

gaa ttt gca gat gct ggc cag tat acc tgt cat aaa gga ggc gag gtt      288
Glu Phe Ala Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Glu Val
                85                  90                  95

ctg agc cat tcg ttc ctc ctg ata cac aaa aag gaa gat gga att tgg      336
Leu Ser His Ser Phe Leu Leu Ile His Lys Lys Glu Asp Gly Ile Trp
            100                 105                 110

tcc act gat atc tta agg gaa cag aaa gaa tcc aaa aat aag atc ttt      384
Ser Thr Asp Ile Leu Arg Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe
        115                 120                 125

cta aaa tgt gag gca aag aat tat tct gga cgt ttc acc tgc tgg tgg      432
Leu Lys Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp
    130                 135                 140

ctg acg gca atc agt acc gat ttg aaa ttc act gtc aaa agc agc aga      480
Leu Thr Ala Ile Ser Thr Asp Leu Lys Phe Thr Val Lys Ser Ser Arg
145                 150                 155                 160

ggc tcc tct gac ccc caa ggg gtg act tgt gga gca gcg aca ctc tca      528
Gly Ser Ser Asp Pro Gln Gly Val Thr Cys Gly Ala Ala Thr Leu Ser
                165                 170                 175

gca gag aag gtc aga gtg gac aac agg gat tat aag aag tac aca gtg      576
Ala Glu Lys Val Arg Val Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val
            180                 185                 190

gag tgt cag gag ggc agt gcc tgc ccg gct gcc gag gag agc cta ccc      624
Glu Cys Gln Glu Gly Ser Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro
        195                 200                 205

att gaa gtc gtg gtg gac gct att cac aag ctc aag tac gaa aac tac      672
Ile Glu Val Val Val Asp Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr
    210                 215                 220

acc agc agc ttc ttc atc agg gac atc atc aaa ccg gac cca ccc aag      720
Thr Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys
225                 230                 235                 240

aac ctg caa ctg aag cca tta aaa aat tct cgg cat gtg gaa gtg agc      768
Asn Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg His Val Glu Val Ser
                245                 250                 255

tgg gaa tac cct gac acc tgg agc acc cca cat tcc tac ttc tcc tta      816
Trp Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu
            260                 265                 270

aca ttt ggc gta cag gtc cag ggc aag aac aac aga gaa aag aaa gac      864
Thr Phe Gly Val Gln Val Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp
        275                 280                 285

aga ctc tcc gtg gac aag acc tca gcc aag gtc gtg tgc cac aag gat      912
Arg Leu Ser Val Asp Lys Thr Ser Ala Lys Val Val Cys His Lys Asp
    290                 295                 300

gcc aag atc cgc gtg caa gcc aga gac cgc tac tat agc tca tcc tgg      960
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Ala Lys Ile Arg Val Gln Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp
305 310 315 320

agc aac tgg gca tcc gtg tcc tgc a 985
Ser Asn Trp Ala Ser Val Ser Cys
325

<210> 56
<211> 328
<212> PRT
<213> Felis catus

<400> 56

Met His Pro Gln Gln Leu Val Ile Ala Trp Phe Ser Leu Val Leu Leu
1 5 10 15

Ala Pro Pro Leu Met Ala Ile Trp Glu Leu Glu Lys Asn Val Tyr Val
20 25 30

Val Glu Leu Asp Trp His Pro Asp Ala Pro Gly Glu Met Val Val Leu
35 40 45

Thr Cys Asn Thr Pro Glu Glu Asp Asp Ile Thr Trp Thr Ser Asp Gln
50 55 60

Ser Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys
65 70 75 80

Glu Phe Ala Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Glu Val
85 90 95

Leu Ser His Ser Phe Leu Leu Ile His Lys Lys Glu Asp Gly Ile Trp
100 105 110

Ser Thr Asp Ile Leu Arg Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe
115 120 125

Leu Lys Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp
130 135 140

Leu Thr Ala Ile Ser Thr Asp Leu Lys Phe Thr Val Lys Ser Ser Arg
145 150 155 160

Gly Ser Ser Asp Pro Gln Gly Val Thr Cys Gly Ala Ala Thr Leu Ser
165 170 175

Ala Glu Lys Val Arg Val Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val
180 185 190

Glu Cys Gln Glu Gly Ser Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro
195 200 205

Ile Glu Val Val Val Asp Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr
210 215 220

Thr Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys
225 230 235 240

Asn Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg His Val Glu Val Ser
245 250 255

Trp Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu
260 265 270

Thr Phe Gly Val Gln Val Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp
275 280 285

Arg Leu Ser Val Asp Lys Thr Ser Ala Lys Val Val Cys His Lys Asp
290 295 300

Ala Lys Ile Arg Val Gln Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp
305 310 315 320

Ser Asn Trp Ala Ser Val Ser Cys
325

<210> 57
<211> 985
<212> DNA
<213> Felis catus

<400> 57
tgcaggacac ggatgcccag ttgctccagg atgagctata gtagcggtct ctggcttgca 60

cgcggatctt ggcatccttg tggcacacga ccttggctga ggtcttgtcc acggagagtc 120

tgtctttctt ttctctgttg ttcttgccct ggacctgtac gccaaatgtt aaggagaagt 180

aggaatgtgg ggtgctccag gtgtcagggt attcccagct cacttccaca tgccgagaat 240

tttttaatgg cttcagttgc aggttcttgg gtgggtccgg tttgatgatg tccctgatga 300

agaagctgct ggtgtagttt tcgtacttga gcttgtgaat agcgtccacc acgacttcaa 360

tgggtaggct ctcctcggca gccgggcagg cactgccctc ctgacactcc actgtgtact 420

tcttataatc cctgttgtcc actctgacct tctctgctga gagtgtcgct gctccacaag 480

tcacccctg ggggtcagag gagcctctgc tgcttttgac agtgaatttc aaatcggtac 540

tgattgccgt cagccaccag caggtgaaac gtccagaata attctttgcc tcacatttta 600

gaaagatctt atttttggat tctttctgtt cccttaagat atcagtggac caaattccat 660

cttccttttt gtgtatcagg aggaacgaat ggctcagaac ctcgcctcct ttatgacagg 720

tatactggcc agcatctgca aattctttga cttggatggt cagagtttta ccagagccta 780

ggacttcact gctctggtca gaggtccagg tgatgtcatc ttcttcagga gtattgcagg 840

tgaggaccac catttctccg ggggcatcag ggtgccagtc caactctaca acataaacgt 900

ttttctccag ttcccatatg gccatgaggg gaggtgccag caaaaccagg gaaaaccagg 960

cgatgaccaa ctgctgagga tgcat 985

<210> 58
<211> 987
<212> DNA
<213> Canis familiaris

<220>
<221> CDS
<222> (1)..(987)
<223>

<400> 58

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atg cac cct cag cag ttg gtc atc tcc tgg ttt tcc ctc gtt ttg ctg       48
Met His Pro Gln Gln Leu Val Ile Ser Trp Phe Ser Leu Val Leu Leu
1               5                   10                  15

gcg tct ccc ctc atg gcc ata tgg gaa ctg gag aaa gat gtt tat gtt       96
Ala Ser Pro Leu Met Ala Ile Trp Glu Leu Glu Lys Asp Val Tyr Val
            20                  25                  30

gta gag ttg gac tgg cac cct gat gcc ccc gga gaa atg gtg gtc ctc      144
Val Glu Leu Asp Trp His Pro Asp Ala Pro Gly Glu Met Val Val Leu
        35                  40                  45

acc tgc cat acc cct gaa gaa gat gac atc act tgg acc tca gcg cag      192
Thr Cys His Thr Pro Glu Glu Asp Asp Ile Thr Trp Thr Ser Ala Gln
    50                  55                  60

agc agt gaa gtc cta ggt tct ggt aaa act ctg acc atc caa gtc aaa      240
Ser Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys
65                  70                  75                  80

gaa ttt gga gat gct ggc cag tat acc tgc cat aaa gga ggc aag gtt      288
Glu Phe Gly Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Lys Val
                85                  90                  95

ctg agc cgc tca ctc ctg ttg att cac aaa aaa gaa gat gga att tgg      336
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Leu Ser Arg Ser Leu Leu Leu Ile His Lys Lys Glu Asp Gly Ile Trp
            100                 105                 110

tcc act gat atc tta aag gaa cag aaa gaa tcc aaa aat aag atc ttt      384
Ser Thr Asp Ile Leu Lys Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe
        115                 120                 125

ctg aaa tgt gag gca aag aat tat tct gga cgt ttc aca tgc tgg tgg      432
Leu Lys Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp
    130                 135                 140

ctg acg gca atc agt act gat ttg aaa ttc agt gtc aaa agt agc aga      480
Leu Thr Ala Ile Ser Thr Asp Leu Lys Phe Ser Val Lys Ser Ser Arg
145                 150                 155                 160

ggc ttc tct gac ccc caa ggg gtg aca tgt gga gca gtg aca ctt tca      528
Gly Phe Ser Asp Pro Gln Gly Val Thr Cys Gly Ala Val Thr Leu Ser
                165                 170                 175

gca gag agg gtc aga gtg gac aac agg gat tat aag aag tac aca gtg      576
Ala Glu Arg Val Arg Val Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val
            180                 185                 190

gag tgt cag gag ggc agt gcc tgc ccc tct gcc gag gag agc cta ccc      624
Glu Cys Gln Glu Gly Ser Ala Cys Pro Ser Ala Glu Glu Ser Leu Pro
        195                 200                 205

atc gag gtc gtg gtg gat gct att cac aag ctc aag tat gaa aac tac      672
Ile Glu Val Val Val Asp Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr
    210                 215                 220

acc agc agc ttc ttc atc aga gac atc atc aaa cca gac cca ccc aca      720
Thr Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Thr
225                 230                 235                 240

aac ctg cag ctg aag cca ttg aaa aat tct cgg cac gtg gag gtc agc      768
Asn Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg His Val Glu Val Ser
                245                 250                 255

tgg gaa tac ccc gac acc tgg agc acc cca cat tcc tac ttc tcc ctg      816
Trp Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu
            260                 265                 270

aca ttt tgc ata cag gcc cag ggc aag aac aat aga gaa aag aaa gat      864
Thr Phe Cys Ile Gln Ala Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp
        275                 280                 285

aga ctc tgc gtg gac aag acc tca gcc aag gtc gtg tgc cac aag gat      912
Arg Leu Cys Val Asp Lys Thr Ser Ala Lys Val Val Cys His Lys Asp
    290                 295                 300

gcc aag atc cgc gtg caa gcc cga gac cgc tac tat agt tca tcc tgg      960
Ala Lys Ile Arg Val Gln Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp
305                 310                 315                 320

agc gac tgg gca tct gtg tca tgc agt                                  987
Ser Asp Trp Ala Ser Val Ser Cys Ser
                325
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<210> 59
<211> 329
<212> PRT
<213> Canis familiaris

<400> 59

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Met His Pro Gln Gln Leu Val Ile Ser Trp Phe Ser Leu Val Leu Leu
1               5                  10                  15

Ala Ser Pro Leu Met Ala Ile Trp Glu Leu Glu Lys Asp Val Tyr Val
            20                  25                  30

Val Glu Leu Asp Trp His Pro Asp Ala Pro Gly Glu Met Val Val Leu
        35                  40                  45

Thr Cys His Thr Pro Glu Glu Asp Asp Ile Thr Trp Thr Ser Ala Gln
    50                  55                  60

Ser Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys
65                  70                  75                  80

Glu Phe Gly Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Lys Val
                85                  90                  95

Leu Ser Arg Ser Leu Leu Leu Ile His Lys Lys Glu Asp Gly Ile Trp
            100                 105                 110

Ser Thr Asp Ile Leu Lys Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe
        115                 120                 125

Leu Lys Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp
    130                 135                 140

Leu Thr Ala Ile Ser Thr Asp Leu Lys Phe Ser Val Lys Ser Ser Arg
145                 150                 155                 160

Gly Phe Ser Asp Pro Gln Gly Val Thr Cys Gly Ala Val Thr Leu Ser
                165                 170                 175

Ala Glu Arg Val Arg Val Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val
            180                 185                 190

Glu Cys Gln Glu Gly Ser Ala Cys Pro Ser Ala Glu Glu Ser Leu Pro
        195                 200                 205
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Ile Glu Val Val Val Asp Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr
210 215 220

Thr Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Thr
225 230 235 240

Asn Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg His Val Glu Val Ser
245 250 255

Trp Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu
260 265 270

Thr Phe Cys Ile Gln Ala Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp
275 280 285

Arg Leu Cys Val Asp Lys Thr Ser Ala Lys Val Val Cys His Lys Asp
290 295 300

Ala Lys Ile Arg Val Gln Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp
305 310 315 320

Ser Asp Trp Ala Ser Val Ser Cys Ser
325

<210> 60
<211> 987
<212> DNA
<213> Canis familiaris

<400> 60
actgcatgac acagatgccc agtcgctcca ggatgaacta tagtagcggt ctcgggcttg 60

cacgcggatc ttggcatcct tgtggcacac gaccttggct gaggtcttgt ccacgcagag 120

tctatctttc ttttctctat tgttcttgcc ctgggcctgt atgcaaaatg tcagggagaa 180

gtaggaatgt ggggtgctcc aggtgtcggg gtattcccag ctgacctcca cgtgccgaga 240

atttttcaat ggcttcagct gcaggtttgt gggtgggtct ggtttgatga tgtctctgat 300

gaagaagctg ctggtgtagt tttcatactt gagcttgtga atagcatcca ccacgacctc 360

gatgggtagg ctctcctcgg cagaggggca ggcactgccc tcctgacact ccactgtgta 420

cttcttataa tccctgttgt ccactctgac cctctctgct gaaagtgtca ctgctccaca 480

tgtcaccccct tgggggtcag agaagcctct gctacttttg acactgaatt tcaaatcagt 540

actgattgcc gtcagccacc agcatgtgaa acgtccagaa taattctttg cctcacattt 600

cagaaagatc ttatttttgg attctttctg ttcctttaag atatcagtgg accaaattcc 660

atcttctttt ttgtgaatca acaggagtga gcggctcaga accttgcctc ctttatggca 720

ggtatactgg ccagcatctc caaattcttt gacttggatg gtcagagttt taccagaacc 780

taggacttca ctgctctgcg ctgaggtcca agtgatgtca tcttcttcag gggtatggca 840

ggtgaggacc accatttctc cgggggcatc agggtgccag tccaactcta caacataaac 900

atctttctcc agttcccata tggccatgag gggagacgcc agcaaaacga gggaaaacca 960

ggagatgacc aactgctgag ggtgcat 987

<210> 61
<211> 1599
<212> DNA
<213> Canis familiaris

<220>
<221> CDS
<222> (1)..(1599)
<223>

<400> 61

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atg cac cct cag cag ttg gtc atc tcc tgg ttt tcc ctc gtt ttg ctg      48
Met His Pro Gln Gln Leu Val Ile Ser Trp Phe Ser Leu Val Leu Leu
1               5                   10                  15

gcg tct ccc ctc atg gcc ata tgg gaa ctg gag aaa gat gtt tat gtt      96
Ala Ser Pro Leu Met Ala Ile Trp Glu Leu Glu Lys Asp Val Tyr Val
            20                  25                  30

gta gag ttg gac tgg cac cct gat gcc ccc gga gaa atg gtg gtc ctc     144
Val Glu Leu Asp Trp His Pro Asp Ala Pro Gly Glu Met Val Val Leu
        35                  40                  45

acc tgc cat acc cct gaa gaa gat gac atc act tgg acc tca gcg cag     192
Thr Cys His Thr Pro Glu Glu Asp Asp Ile Thr Trp Thr Ser Ala Gln
    50                  55                  60

agc agt gaa gtc cta ggt tct ggt aaa act ctg acc atc caa gtc aaa     240
Ser Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys
65                  70                  75                  80

gaa ttt gga gat gct ggc cag tat acc tgc cat aaa gga ggc aag gtt     288
Glu Phe Gly Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Lys Val
                85                  90                  95

ctg agc cgc tca ctc ctg ttg att cac aaa aaa gaa gat gga att tgg     336
Leu Ser Arg Ser Leu Leu Leu Ile His Lys Lys Glu Asp Gly Ile Trp
            100                 105                 110

tcc act gat atc tta aag gaa cag aaa gaa tcc aaa aat aag atc ttt     384
Ser Thr Asp Ile Leu Lys Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe
        115                 120                 125
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ctg aaa tgt gag gca aag aat tat tct gga cgt ttc aca tgc tgg tgg      432
Leu Lys Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp
    130                 135                 140

ctg acg gca atc agt act gat ttg aaa ttc agt gtc aaa agt agc aga      480
Leu Thr Ala Ile Ser Thr Asp Leu Lys Phe Ser Val Lys Ser Ser Arg
145                 150                 155                 160

ggc ttc tct gac ccc caa ggg gtg aca tgt gga gca gtg aca ctt tca      528
Gly Phe Ser Asp Pro Gln Gly Val Thr Cys Gly Ala Val Thr Leu Ser
                165                 170                 175

gca gag agg gtc aga gtg gac aac agg gat tat aag aag tac aca gtg      576
Ala Glu Arg Val Arg Val Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val
            180                 185                 190

gag tgt cag gag ggc agt gcc tgc ccc tct gcc gag gag agc cta ccc      624
Glu Cys Gln Glu Gly Ser Ala Cys Pro Ser Ala Glu Glu Ser Leu Pro
        195                 200                 205

atc gag gtc gtg gtg gat gct att cac aag ctc aag tat gaa aac tac      672
Ile Glu Val Val Val Asp Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr
    210                 215                 220

acc agc agc ttc ttc atc aga gac atc atc aaa cca gac cca ccc aca      720
Thr Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Thr
225                 230                 235                 240

aac ctg cag ctg aag cca ttg aaa aat tct cgg cac gtg gag gtc agc      768
Asn Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg His Val Glu Val Ser
                245                 250                 255

tgg gaa tac ccc gac acc tgg agc acc cca cat tcc tac ttc tcc ctg      816
Trp Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu
            260                 265                 270

aca ttt tgc ata cag gcc cag ggc aag aac aat aga gaa aag aaa gat      864
Thr Phe Cys Ile Gln Ala Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp
        275                 280                 285

aga ctc tgc gtg gac aag acc tca gcc aag gtc gtg tgc cac aag gat      912
Arg Leu Cys Val Asp Lys Thr Ser Ala Lys Val Val Cys His Lys Asp
    290                 295                 300

gcc aag atc cgc gtg caa gcc cga gac cgc tac tat agt tca tcc tgg      960
Ala Lys Ile Arg Val Gln Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp
305                 310                 315                 320

agc gac tgg gca tct gtg tca tgc agt ggt ggc ggt ggc ggc gga tct     1008
Ser Asp Trp Ala Ser Val Ser Cys Ser Gly Gly Gly Gly Gly Gly Ser
                325                 330                 335

aga aac ttg cca acc cct act cca tcc ccg ggt atg ttc caa tgt ttg     1056
Arg Asn Leu Pro Thr Pro Thr Pro Ser Pro Gly Met Phe Gln Cys Leu
            340                 345                 350

aac cac tcc caa acc ttg ttg aga gcc gtc agc aac acg ctt cag aag     1104
Asn His Ser Gln Thr Leu Leu Arg Ala Val Ser Asn Thr Leu Gln Lys
        355                 360                 365
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gcc aga caa act cta gaa tta tat tcc tgc act tcc gaa gag att gat     1152
Ala Arg Gln Thr Leu Glu Leu Tyr Ser Cys Thr Ser Glu Glu Ile Asp
    370                 375                 380

cat gaa gat atc aca aag gat aaa acc agc aca gtg gag gcc tgc tta     1200
His Glu Asp Ile Thr Lys Asp Lys Thr Ser Thr Val Glu Ala Cys Leu
385                 390                 395                 400

cca ctg gaa tta acc atg aat gag agt tgc ctg gct tcc aga gag atc     1248
Pro Leu Glu Leu Thr Met Asn Glu Ser Cys Leu Ala Ser Arg Glu Ile
                405                 410                 415

tct ttg ata act aac ggg agt tgc ctg gcc tct gga aag gcc tct ttt     1296
Ser Leu Ile Thr Asn Gly Ser Cys Leu Ala Ser Gly Lys Ala Ser Phe
            420                 425                 430

atg acg gtc ctg tgc ctt agc agc atc tat gag gac ttg aag atg tac     1344
Met Thr Val Leu Cys Leu Ser Ser Ile Tyr Glu Asp Leu Lys Met Tyr
        435                 440                 445

cag atg gaa ttc aag gcc atg aac gca aag ctt tta atg gat ccc aag     1392
Gln Met Glu Phe Lys Ala Met Asn Ala Lys Leu Leu Met Asp Pro Lys
    450                 455                 460

agg cag atc ttt ctg gat caa aac atg ctg aca gct atc gat gag ctg     1440
Arg Gln Ile Phe Leu Asp Gln Asn Met Leu Thr Ala Ile Asp Glu Leu
465                 470                 475                 480

tta cag gcc ctg aat ttc aac agt gtg act gtg cca cag aaa tcc tcc     1488
Leu Gln Ala Leu Asn Phe Asn Ser Val Thr Val Pro Gln Lys Ser Ser
                485                 490                 495

ctt gaa gag ccg gat ttt tat aaa act aaa atc aag ctc tgc ata ctt     1536
Leu Glu Glu Pro Asp Phe Tyr Lys Thr Lys Ile Lys Leu Cys Ile Leu
            500                 505                 510

ctt cat gct ttc aga att cgt gcg gtg acc atc aat aga atg atg tcc     1584
Leu His Ala Phe Arg Ile Arg Ala Val Thr Ile Asn Arg Met Met Ser
        515                 520                 525

tac ttg aac tct tcc                                                 1599
Tyr Leu Asn Ser Ser
    530
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<210> 62
<211> 533
<212> PRT
<213> Canis familiaris

<400> 62

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Met His Pro Gln Gln Leu Val Ile Ser Trp Phe Ser Leu Val Leu Leu
1               5                   10                  15

Ala Ser Pro Leu Met Ala Ile Trp Glu Leu Glu Lys Asp Val Tyr Val
            20                  25                  30
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Val Glu Leu Asp Trp His Pro Asp Ala Pro Gly Glu Met Val Val Leu
        35                  40                  45

Thr Cys His Thr Pro Glu Glu Asp Asp Ile Thr Trp Thr Ser Ala Gln
    50                  55                  60

Ser Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys
65                  70                  75                  80

Glu Phe Gly Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Lys Val
                85                  90                  95

Leu Ser Arg Ser Leu Leu Leu Ile His Lys Lys Glu Asp Gly Ile Trp
            100                 105                 110

Ser Thr Asp Ile Leu Lys Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe
        115                 120                 125

Leu Lys Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp
    130                 135                 140

Leu Thr Ala Ile Ser Thr Asp Leu Lys Phe Ser Val Lys Ser Ser Arg
145                 150                 155                 160

Gly Phe Ser Asp Pro Gln Gly Val Thr Cys Gly Ala Val Thr Leu Ser
                165                 170                 175

Ala Glu Arg Val Arg Val Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val
            180                 185                 190

Glu Cys Gln Glu Gly Ser Ala Cys Pro Ser Ala Glu Glu Ser Leu Pro
        195                 200                 205

Ile Glu Val Val Val Asp Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr
    210                 215                 220

Thr Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Thr
225                 230                 235                 240

Asn Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg His Val Glu Val Ser
                245                 250                 255

Trp Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu
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260 265 270

Thr Phe Cys Ile Gln Ala Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp
275 280 285

Arg Leu Cys Val Asp Lys Thr Ser Ala Lys Val Val Cys His Lys Asp
290 295 300

Ala Lys Ile Arg Val Gln Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp
305 310 315 320

Ser Asp Trp Ala Ser Val Ser Cys Ser Gly Gly Gly Gly Gly Gly Ser
325 330 335

Arg Asn Leu Pro Thr Pro Thr Pro Ser Pro Gly Met Phe Gln Cys Leu
340 345 350

Asn His Ser Gln Thr Leu Leu Arg Ala Val Ser Asn Thr Leu Gln Lys
355 360 365

Ala Arg Gln Thr Leu Glu Leu Tyr Ser Cys Thr Ser Glu Glu Ile Asp
370 375 380

His Glu Asp Ile Thr Lys Asp Lys Thr Ser Thr Val Glu Ala Cys Leu
385 390 395 400

Pro Leu Glu Leu Thr Met Asn Glu Ser Cys Leu Ala Ser Arg Glu Ile
405 410 415

Ser Leu Ile Thr Asn Gly Ser Cys Leu Ala Ser Gly Lys Ala Ser Phe
420 425 430

Met Thr Val Leu Cys Leu Ser Ser Ile Tyr Glu Asp Leu Lys Met Tyr
435 440 445

Gln Met Glu Phe Lys Ala Met Asn Ala Lys Leu Leu Met Asp Pro Lys
450 455 460

Arg Gln Ile Phe Leu Asp Gln Asn Met Leu Thr Ala Ile Asp Glu Leu
465 470 475 480

Leu Gln Ala Leu Asn Phe Asn Ser Val Thr Val Pro Gln Lys Ser Ser
485 490 495

Leu Glu Glu Pro Asp Phe Tyr Lys Thr Lys Ile Lys Leu Cys Ile Leu
500 505 510

Leu His Ala Phe Arg Ile Arg Ala Val Thr Ile Asn Arg Met Met Ser
515 520 525

Tyr Leu Asn Ser Ser
530

<210> 63
<211> 1599
<212> DNA
<213> Canis familiaris

<400> 63
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aagaagtatg cagagcttga ttttagtttt ataaaaatcc ggctcttcaa gggaggattt 120

ctgtggcaca gtcacactgt tgaaattcag ggcctgtaac agctcatcga tagctgtcag 180

catgttttga tccagaaaga tctgcctctt gggatccatt aaaagctttg cgttcatggc 240

cttgaattcc atctggtaca tcttcaagtc ctcatagatg ctgctaaggc acaggaccgt 300

cataaaagag gcctttccag aggccaggca actcccgtta gttatcaaag agatctctct 360

ggaagccagg caactctcat tcatggttaa ttccagtggt aagcaggcct ccactgtgct 420

ggttttatcc tttgtgatat cttcatgatc aatctcttcg gaagtgcagg aatataattc 480

tagagtttgt ctggccttct gaagcgtgtt gctgacggct ctcaacaagg tttgggagtg 540

gttcaaacat tggaacatac ccggggatgg agtaggggtt ggcaagtttc tagatccgcc 600

gccaccgcca ccactgcatg acacagatgc ccagtcgctc caggatgaac tatagtagcg 660

gtctcgggct tgcacgcgga tcttggcatc cttgtggcac acgaccttgg ctgaggtctt 720

gtccacgcag agtctatctt tcttttctct attgttcttg ccctgggcct gtatgcaaaa 780

tgtcagggag aagtaggaat gtggggtgct ccaggtgtcg gggtattccc agctgacctc 840

cacgtgccga gaatttttca atggcttcag ctgcaggttt gtgggtgggt ctggtttgat 900

gatgtctctg atgaagaagc tgctggtgta gttttcatac ttgagcttgt gaatagcatc 960

caccacgacc tcgatgggta ggctctcctc ggcagagggg caggcactgc cctcctgaca 1020

ctccactgtg tacttcttat aatccctgtt gtccactctg accctctctg ctgaaagtgt 1080

cactgctcca catgtcaccc cttgggggtc agagaagcct ctgctacttt tgacactgaa 1140

tttcaaatca gtactgattg ccgtcagcca ccagcatgtg aaacgtccag aataattctt 1200

tgcctcacat ttcagaaaga tcttattttt ggattctttc tgttccttta agatatcagt 1260

ggaccaaatt ccatcttctt ttttgtgaat caacaggagt gagcggctca gaaccttgcc 1320

tcctttatgg caggtatact ggccagcatc tccaaattct ttgacttgga tggtcagagt 1380

tttaccagaa cctaggactt cactgctctg cgctgaggtc caagtgatgt catcttcttc 1440

aggggtatgg caggtgagga ccaccatttc tccgggggca tcagggtgcc agtccaactc 1500

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gagggaaaac caggagatga ccaactgctg agggtgcat 1599

<210> 64
<211> 0
<212> DNA
<213> Canis familiaris

<400> 64
000

<210> 65
<211> 0
<212> DNA
<213> Canis familiaris

<400> 65
000

<210> 66
<211> 1533
<212> DNA
<213> Canis familiaris

<220>
<221> CDS
<222> (1)..(1533)
<223>

<400> 66

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1               5                  10                  15

cct gat gcc ccc gga gaa atg gtg gtc ctc acc tgc cat acc cct gaa       96
Pro Asp Ala Pro Gly Glu Met Val Val Leu Thr Cys His Thr Pro Glu
            20                  25                  30

gaa gat gac atc act tgg acc tca gcg cag agc agt gaa gtc cta ggt      144
Glu Asp Asp Ile Thr Trp Thr Ser Ala Gln Ser Ser Glu Val Leu Gly
        35                  40                  45

tct ggt aaa act ctg acc atc caa gtc aaa gaa ttt gga gat gct ggc      192
Ser Gly Lys Thr Leu Thr Ile Gln Val Lys Glu Phe Gly Asp Ala Gly
    50                  55                  60

cag tat acc tgc cat aaa gga ggc aag gtt ctg agc cgc tca ctc ctg      240
```

```
Gln Tyr Thr Cys His Lys Gly Gly Lys Val Leu Ser Arg Ser Leu Leu
65                  70                  75                  80

ttg att cac aaa aaa gaa gat gga att tgg tcc act gat atc tta aag      288
Leu Ile His Lys Lys Glu Asp Gly Ile Trp Ser Thr Asp Ile Leu Lys
                85                  90                  95

gaa cag aaa gaa tcc aaa aat aag atc ttt ctg aaa tgt gag gca aag      336
Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe Leu Lys Cys Glu Ala Lys
            100                 105                 110

aat tat tct gga cgt ttc aca tgc tgg tgg ctg acg gca atc agt act      384
Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp Leu Thr Ala Ile Ser Thr
        115                 120                 125

gat ttg aaa ttc agt gtc aaa agt agc aga ggc ttc tct gac ccc caa      432
Asp Leu Lys Phe Ser Val Lys Ser Ser Arg Gly Phe Ser Asp Pro Gln
    130                 135                 140

ggg gtg aca tgt gga gca gtg aca ctt tca gca gag agg gtc aga gtg      480
Gly Val Thr Cys Gly Ala Val Thr Leu Ser Ala Glu Arg Val Arg Val
145                 150                 155                 160

gac aac agg gat tat aag aag tac aca gtg gag tgt cag gag ggc agt      528
Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val Glu Cys Gln Glu Gly Ser
                165                 170                 175

gcc tgc ccc tct gcc gag gag agc cta ccc atc gag gtc gtg gtg gat      576
Ala Cys Pro Ser Ala Glu Glu Ser Leu Pro Ile Glu Val Val Val Asp
            180                 185                 190

gct att cac aag ctc aag tat gaa aac tac acc agc agc ttc ttc atc      624
Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr Thr Ser Ser Phe Phe Ile
        195                 200                 205

aga gac atc atc aaa cca gac cca ccc aca aac ctg cag ctg aag cca      672
Arg Asp Ile Ile Lys Pro Asp Pro Pro Thr Asn Leu Gln Leu Lys Pro
    210                 215                 220

ttg aaa aat tct cgg cac gtg gag gtc agc tgg gaa tac ccc gac acc      720
Leu Lys Asn Ser Arg His Val Glu Val Ser Trp Glu Tyr Pro Asp Thr
225                 230                 235                 240

tgg agc acc cca cat tcc tac ttc tcc ctg aca ttt tgc ata cag gcc      768
Trp Ser Thr Pro His Ser Tyr Phe Ser Leu Thr Phe Cys Ile Gln Ala
                245                 250                 255

cag ggc aag aac aat aga gaa aag aaa gat aga ctc tgc gtg gac aag      816
Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp Arg Leu Cys Val Asp Lys
            260                 265                 270

acc tca gcc aag gtc gtg tgc cac aag gat gcc aag atc cgc gtg caa      864
Thr Ser Ala Lys Val Val Cys His Lys Asp Ala Lys Ile Arg Val Gln
        275                 280                 285

gcc cga gac cgc tac tat agt tca tcc tgg agc gac tgg gca tct gtg      912
Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp Ser Asp Trp Ala Ser Val
    290                 295                 300
```

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tca tgc agt ggt ggc ggt ggc ggc gga tct aga aac ttg cca acc cct      960
Ser Cys Ser Gly Gly Gly Gly Gly Gly Ser Arg Asn Leu Pro Thr Pro
305                 310                 315                 320

act cca tcc ccg ggt atg ttc caa tgt ttg aac cac tcc caa acc ttg     1008
Thr Pro Ser Pro Gly Met Phe Gln Cys Leu Asn His Ser Gln Thr Leu
                325                 330                 335

ttg aga gcc gtc agc aac acg ctt cag aag gcc aga caa act cta gaa     1056
Leu Arg Ala Val Ser Asn Thr Leu Gln Lys Ala Arg Gln Thr Leu Glu
            340                 345                 350

tta tat tcc tgc act tcc gaa gag att gat cat gaa gat atc aca aag     1104
Leu Tyr Ser Cys Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys
        355                 360                 365

gat aaa acc agc aca gtg gag gcc tgc tta cca ctg gaa tta acc atg     1152
Asp Lys Thr Ser Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Thr Met
    370                 375                 380

aat gag agt tgc ctg gct tcc aga gag atc tct ttg ata act aac ggg     1200
Asn Glu Ser Cys Leu Ala Ser Arg Glu Ile Ser Leu Ile Thr Asn Gly
385                 390                 395                 400

agt tgc ctg gcc tct gga aag gcc tct ttt atg acg gtc ctg tgc ctt     1248
Ser Cys Leu Ala Ser Gly Lys Ala Ser Phe Met Thr Val Leu Cys Leu
                405                 410                 415

agc agc atc tat gag gac ttg aag atg tac cag atg gaa ttc aag gcc     1296
Ser Ser Ile Tyr Glu Asp Leu Lys Met Tyr Gln Met Glu Phe Lys Ala
            420                 425                 430

atg aac gca aag ctt tta atg gat ccc aag agg cag atc ttt ctg gat     1344
Met Asn Ala Lys Leu Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp
        435                 440                 445

caa aac atg ctg aca gct atc gat gag ctg tta cag gcc ctg aat ttc     1392
Gln Asn Met Leu Thr Ala Ile Asp Glu Leu Leu Gln Ala Leu Asn Phe
    450                 455                 460

aac agt gtg act gtg cca cag aaa tcc tcc ctt gaa gag ccg gat ttt     1440
Asn Ser Val Thr Val Pro Gln Lys Ser Ser Leu Glu Glu Pro Asp Phe
465                 470                 475                 480

tat aaa act aaa atc aag ctc tgc ata ctt ctt cat gct ttc aga att     1488
Tyr Lys Thr Lys Ile Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile
                485                 490                 495

cgt gcg gtg acc atc aat aga atg atg tcc tac ttg aac tct tcc         1533
Arg Ala Val Thr Ile Asn Arg Met Met Ser Tyr Leu Asn Ser Ser
            500                 505                 510
```

<210> 67
<211> 511
<212> PRT
<213> Canis familiaris

<400> 67

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Ile Trp Glu Leu Glu Lys Asp Val Tyr Val Val Glu Leu Asp Trp His
1               5                  10                  15

Pro Asp Ala Pro Gly Glu Met Val Val Leu Thr Cys His Thr Pro Glu
            20                  25                  30

Glu Asp Asp Ile Thr Trp Thr Ser Ala Gln Ser Ser Glu Val Leu Gly
        35                  40                  45

Ser Gly Lys Thr Leu Thr Ile Gln Val Lys Glu Phe Gly Asp Ala Gly
    50                  55                  60

Gln Tyr Thr Cys His Lys Gly Gly Lys Val Leu Ser Arg Ser Leu Leu
65                  70                  75                  80

Leu Ile His Lys Lys Glu Asp Gly Ile Trp Ser Thr Asp Ile Leu Lys
                85                  90                  95

Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe Leu Lys Cys Glu Ala Lys
            100                 105                 110

Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp Leu Thr Ala Ile Ser Thr
        115                 120                 125

Asp Leu Lys Phe Ser Val Lys Ser Ser Arg Gly Phe Ser Asp Pro Gln
    130                 135                 140

Gly Val Thr Cys Gly Ala Val Thr Leu Ser Ala Glu Arg Val Arg Val
145                 150                 155                 160

Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val Glu Cys Gln Glu Gly Ser
                165                 170                 175

Ala Cys Pro Ser Ala Glu Glu Ser Leu Pro Ile Glu Val Val Val Asp
            180                 185                 190

Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr Thr Ser Ser Phe Phe Ile
        195                 200                 205

Arg Asp Ile Ile Lys Pro Asp Pro Pro Thr Asn Leu Gln Leu Lys Pro
    210                 215                 220

Leu Lys Asn Ser Arg His Val Glu Val Ser Trp Glu Tyr Pro Asp Thr
225                 230                 235                 240
```

```
Trp Ser Thr Pro His Ser Tyr Phe Ser Leu Thr Phe Cys Ile Gln Ala
                245                 250                 255

Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp Arg Leu Cys Val Asp Lys
            260                 265                 270

Thr Ser Ala Lys Val Val Cys His Lys Asp Ala Lys Ile Arg Val Gln
        275                 280                 285

Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp Ser Asp Trp Ala Ser Val
    290                 295                 300

Ser Cys Ser Gly Gly Gly Gly Gly Gly Ser Arg Asn Leu Pro Thr Pro
305                 310                 315                 320

Thr Pro Ser Pro Gly Met Phe Gln Cys Leu Asn His Ser Gln Thr Leu
                325                 330                 335

Leu Arg Ala Val Ser Asn Thr Leu Gln Lys Ala Arg Gln Thr Leu Glu
            340                 345                 350

Leu Tyr Ser Cys Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys
        355                 360                 365

Asp Lys Thr Ser Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Thr Met
    370                 375                 380

Asn Glu Ser Cys Leu Ala Ser Arg Glu Ile Ser Leu Ile Thr Asn Gly
385                 390                 395                 400

Ser Cys Leu Ala Ser Gly Lys Ala Ser Phe Met Thr Val Leu Cys Leu
                405                 410                 415

Ser Ser Ile Tyr Glu Asp Leu Lys Met Tyr Gln Met Glu Phe Lys Ala
            420                 425                 430

Met Asn Ala Lys Leu Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp
        435                 440                 445

Gln Asn Met Leu Thr Ala Ile Asp Glu Leu Leu Gln Ala Leu Asn Phe
    450                 455                 460

Asn Ser Val Thr Val Pro Gln Lys Ser Ser Leu Glu Glu Pro Asp Phe
```

465 470 475 480

Tyr Lys Thr Lys Ile Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile
485 490 495

Arg Ala Val Thr Ile Asn Arg Met Met Ser Tyr Leu Asn Ser Ser
500 505 510

<210> 68
<211> 1533
<212> DNA
<213> Canis familiaris

<400> 68
ggaagagttc aagtaggaca tcattctatt gatggtcacc gcacgaattc tgaaagcatg 60

aagaagtatg cagagcttga ttttagtttt ataaaaatcc ggctcttcaa gggaggattt 120

ctgtggcaca gtcacactgt tgaaattcag ggcctgtaac agctcatcga tagctgtcag 180

catgttttga tccagaaaga tctgcctctt gggatccatt aaaagctttg cgttcatggc 240

cttgaattcc atctggtaca tcttcaagtc ctcatagatg ctgctaaggc acaggaccgt 300

cataaaagag gcctttccag aggccaggca actcccgtta gttatcaaag agatctctct 360

ggaagccagg caactctcat tcatggttaa ttccagtggt aagcaggcct ccactgtgct 420

ggttttatcc tttgtgatat cttcatgatc aatctcttcg gaagtgcagg aatataattc 480

tagagtttgt ctggccttct gaagcgtgtt gctgacggct ctcaacaagg tttgggagtg 540

gttcaaacat tggaacatac ccggggatgg agtaggggtt ggcaagtttc tagatccgcc 600

gccaccgcca ccactgcatg acacagatgc ccagtcgctc caggatgaac tatagtagcg 660

gtctcgggct tgcacgcgga tcttggcatc cttgtggcac acgaccttgg ctgaggtctt 720

gtccacgcag agtctatctt tcttttctct attgttcttg ccctgggcct gtatgcaaaa 780

tgtcagggag aagtaggaat gtggggtgct ccaggtgtcg gggtattccc agctgacctc 840

cacgtgccga gaatttttca atggcttcag ctgcaggttt gtgggtgggt ctggtttgat 900

gatgtctctg atgaagaagc tgctggtgta gttttcatac ttgagcttgt gaatagcatc 960

caccacgacc tcgatgggta ggctctcctc ggcagagggg caggcactgc cctcctgaca 1020

ctccactgtg tacttcttat aatccctgtt gtccactctg accctctctg ctgaaagtgt 1080

cactgctcca catgtcaccc cttgggggtc agagaagcct ctgctacttt tgacactgaa 1140

tttcaaatca gtactgattg ccgtcagcca ccagcatgtg aaacgtccag aataattctt 1200

tgcctcacat ttcagaaaga tcttattttt ggattctttc tgttccttta agatatcagt 1260

ggaccaaatt ccatcttctt ttttgtgaat caacaggagt gagcggctca gaaccttgcc 1320

tcctttatgg caggtatact ggccagcatc tccaaattct ttgacttgga tggtcagagt 1380

tttaccagaa cctaggactt cactgctctg cgctgaggtc caagtgatgt catcttcttc 1440

aggggtatgg caggtgagga ccaccatttc tccgggggca tcagggtgcc agtccaactc 1500

tacaacataa acatctttct ccagttccca tat 1533

<210> 69
<211> 30
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic Primer

<400> 69
gccaagctcg aaattaaccc tcactaaagg 30

<210> 70
<211> 28
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic Primer

<400> 70
cgacggccag tgaattgtaa tacgactc 28

<210> 71
<211> 31
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic Primer

<400> 71
agtgatgaag gcctggaatc agattacttt g 31

<210> 72
<211> 32
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic Primer

<400> 72
atggcctgga acacttctct gaaagaatat ga 32

<210> 73
<211> 30
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic Primer

<400> 73
aactattgag cacagggata aagatgactg 30

<210> 74
<211> 33
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic Primer

<400> 74
aatatctaat tcttgttttg aacagtgaac att 33

<210> 75
<211> 36
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic Primer

<400> 75
tatgccggct actttggcaa gcttgaacat aaactc 36

<210> 76
<211> 37
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic Primer

<400> 76
ggcctcgagc taattcttgt tttgaacagt gaacatt 37

<210> 77
<211> 28
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic Primer

<400> 77
atggccgaca aggtcctgaa ggagaaga 28

<210> 78
<211> 33
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic Primer

<400> 78
ttaatgtcct gggaagaggt agaaacatct tgt 33

<210> 79
<211> 26
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic Primer

<400> 79
tcaagcccac aatctggaaa ttctca 26

<210> 80
<211> 26
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic Primer

<400> 80
ctggagagtc actgatcaac agttcc 26

<210> 81
<211> 36
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic Primer

<400> 81
acaaggatcc accatggccg acaaggatct gaaggg 36

<210> 82
<211> 39
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic Primer

<400> 82
cgcctctaga cctcaattgc cagggaagag atagaagta 39

<210> 83
<211> 60
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic Primer

<400> 83
ctgcagtggt ggcggtggcg gcggatctag aaacttgcca acccctactc catccccggg 60

<210> 84
<211> 60
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic Primer

<400> 84
cccggggatg gagtaggggt tggcaagttt ctagatccgc cgccaccgcc accactgcag 60

<210> 85
<211> 28
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic Primer

<400> 85
atgcatcctc agcagttggt catcgcct 28

<210> 86
<211> 25
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic Primer

<400> 86
tgcaggacac ggatgcccag ttgct 25

<210> 87
<211> 37
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic Primer

<400> 87

acaggtacca tgcatcctca gcagttggtc atcgcct 37

<210> 88
<211> 25
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic Primer

<400> 88
ctaactgcag gacacggatg cccag 25

<210> 89
<211> 19
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic Primer

<400> 89
atgtgcccgc cgcgtggcc 19

<210> 90
<211> 27
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic Primer

<400> 90
ctaggaagca ttcagatagc tcatcat 27

<210> 91
<211> 39
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic Primer

<400> 91
tatgacccgg ggatgttcca gtgcctcaac cactcccaa 39

<210> 92
<211> 41
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic Primer

<400> 92
atgactgcgg ccgcctagga agcattcaga tagctcatca t 41

<210> 93
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic Primer

<400> 93
ccatcctggt cctgctaagc 20

<210> 94
<211> 22
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic Primer

<400> 94
ccatctggta catcttcaag tc 22

<210> 95
<211> 38
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic Primer

<400> 95
aaaaaacccg ggtatgttcc aatgtttcaa ccactccc 38

<210> 96
<211> 51
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic Primer

<400> 96
gcggccgctc gagttaggaa gagttcaagt aggacatcat tctattgatg g 51

<210> 97
<211> 22
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic Primer

<400> 97
cttaaaggaa cagaaagaat cc 22

<210> 98
<211> 19
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic Primer

<400> 98
ggtattccca gctgacctc 19

<210> 99
<211> 37
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic Primer

<400> 99
cataggtacc atgcaccctc agcagttggt catctcc 37

<210> 100
<211> 29
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic Primer

<400> 100
atctaaatgc atgacacaga tgcccagtc 29

<210> 101
<211> 561
<212> DNA
<213> Felis catus

<220>
<221> CDS
<222> (1)..(561)
<223>

<400> 101
ggg atg ttc cag tgc ctc aac cac tcc caa acc ctg ctg cga gcc atc 48
Gly Met Phe Gln Cys Leu Asn His Ser Gln Thr Leu Leu Arg Ala Ile
1 5 10 15

agc aac acg ctt cag aag gcc aga caa act cta gaa ttt tac tcc tgc 96
Ser Asn Thr Leu Gln Lys Ala Arg Gln Thr Leu Glu Phe Tyr Ser Cys

```
            20                  25                  30

act tcc gaa gag att gat cat gaa gat atc aca aaa gat aaa acc agc      144
Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys Asp Lys Thr Ser
        35                  40                  45

aca gtg gag gcc tgc tta cca ctg gaa tta acc atg aat gag agt tgc      192
Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Thr Met Asn Glu Ser Cys
    50                  55                  60

ctg gct tcc aga gag atc tct ctg ata act aat ggg agt tgc ctg gcc      240
Leu Ala Ser Arg Glu Ile Ser Leu Ile Thr Asn Gly Ser Cys Leu Ala
65                  70                  75                  80

tcc aga aag acc tct ttt atg acg acc ctg tgc ctt agc agt atc tat      288
Ser Arg Lys Thr Ser Phe Met Thr Thr Leu Cys Leu Ser Ser Ile Tyr
                85                  90                  95

gag gac ttg aag atg tac cag gtg gag ttc aag gcc atg aat gca aag      336
Glu Asp Leu Lys Met Tyr Gln Val Glu Phe Lys Ala Met Asn Ala Lys
            100                 105                 110

ctg tta atg gat cct aaa agg cag atc ttt ctg gat caa aac atg ctg      384
Leu Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp Gln Asn Met Leu
        115                 120                 125

aca gct att gat gag ctg tta cag gcc ctg aat gtc aac agt gtg act      432
Thr Ala Ile Asp Glu Leu Leu Gln Ala Leu Asn Val Asn Ser Val Thr
    130                 135                 140

gtg cca cag aac tcc tcc ctg gaa gaa ccg gat ttt tat aaa act aaa      480
Val Pro Gln Asn Ser Ser Leu Glu Glu Pro Asp Phe Tyr Lys Thr Lys
145                 150                 155                 160

atc aag ctc tgc ata ctt ctt cat gct ttc aga att cgt gca gtg acc      528
Ile Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile Arg Ala Val Thr
                165                 170                 175

atc aat aga atg atg agc tat ctg aat gct tcc                          561
Ile Asn Arg Met Met Ser Tyr Leu Asn Ala Ser
            180                 185
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<210> 102
<211> 187
<212> PRT
<213> Felis catus

<400> 102

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Gly Met Phe Gln Cys Leu Asn His Ser Gln Thr Leu Leu Arg Ala Ile
1               5                   10                  15

Ser Asn Thr Leu Gln Lys Ala Arg Gln Thr Leu Glu Phe Tyr Ser Cys
            20                  25                  30

Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys Asp Lys Thr Ser
```

35 40 45

Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Thr Met Asn Glu Ser Cys
50 55 60

Leu Ala Ser Arg Glu Ile Ser Leu Ile Thr Asn Gly Ser Cys Leu Ala
65 70 75 80

Ser Arg Lys Thr Ser Phe Met Thr Thr Leu Cys Leu Ser Ser Ile Tyr
85 90 95

Glu Asp Leu Lys Met Tyr Gln Val Glu Phe Lys Ala Met Asn Ala Lys
100 105 110

Leu Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp Gln Asn Met Leu
115 120 125

Thr Ala Ile Asp Glu Leu Leu Gln Ala Leu Asn Val Asn Ser Val Thr
130 135 140

Val Pro Gln Asn Ser Ser Leu Glu Glu Pro Asp Phe Tyr Lys Thr Lys
145 150 155 160

Ile Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile Arg Ala Val Thr
165 170 175

Ile Asn Arg Met Met Ser Tyr Leu Asn Ala Ser
180 185

<210> 103
<211> 561
<212> DNA
<213> Felis catus

<400> 103
ggaagcattc agatagctca tcattctatt gatggtcact gcacgaattc tgaaagcatg 60

aagaagtatg cagagcttga ttttagtttt ataaaaatcc ggttcttcca gggaggagtt 120

ctgtggcaca gtcacactgt tgacattcag ggcctgtaac agctcatcaa tagctgtcag 180

catgttttga tccagaaaga tctgcctttt aggatccatt aacagctttg cattcatggc 240

cttgaactcc acctggtaca tcttcaagtc ctcatagata ctgctaaggc acagggtcgt 300

cataaaagag gtctttctgg aggccaggca actcccatta gttatcagag agatctctct 360

ggaagccagg caactctcat tcatggttaa ttccagtggt aagcaggcct ccactgtgct 420

ggttttatct tttgtgatat cttcatgatc aatctcttcg gaagtgcagg agtaaaattc 480

tagagtttgt ctggccttct gaagcgtgtt gctgatggct cgcagcaggg tttgggagtg 540

gttgaggcac tggaacatcc c 561

<210> 104
<211> 1455
<212> DNA
<213> Canis familiaris

<220>
<221> CDS
<222> (232)..(897)
<223>

<400> 104
ggcacgaggc aaaccccgcg ggcccagctc cacgtgtcac cgagaagctg atgtagagag 60

agacagagag agaaagcaag ccggacaccg gagtcccggg aaagtcctgg cgcgcctcgg 120

gccaattata aaaatgtgac cccccgggtc ggcctcccac cgccgccctc ccctgccgcg 180

tccgcagtcc gcgtccagcg cccgccgggg tccacgcagc gcccgcccag c atg tgc 237
Met Cys
1

ccg ccg cgc ggc ctc ctc ctt gtg acc atc ctg gtc ctg cta agc cac 285
Pro Pro Arg Gly Leu Leu Leu Val Thr Ile Leu Val Leu Leu Ser His
5 10 15

ctg gac cac ctt act tgg gcc agg agc ctc ccc aca gcc tca ccg agc 333
Leu Asp His Leu Thr Trp Ala Arg Ser Leu Pro Thr Ala Ser Pro Ser
20 25 30

cca gga ata ttc cag tgc ctc aac cac tcc caa aac ctg ctg aga gcc 381
Pro Gly Ile Phe Gln Cys Leu Asn His Ser Gln Asn Leu Leu Arg Ala
35 40 45 50

gtc agc aac acg ctt cag aag gcc aga caa act cta gaa tta tat tcc 429
Val Ser Asn Thr Leu Gln Lys Ala Arg Gln Thr Leu Glu Leu Tyr Ser
55 60 65

tgc act tcc gaa gag att gat cat gaa gat atc aca aag gat aaa acc 477
Cys Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys Asp Lys Thr
70 75 80

agc aca gtg gag gcc tgc tta cca ctg gaa tta acc atg aat gag agt 525
Ser Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Thr Met Asn Glu Ser
85 90 95

tgc ctg gct tcc aga gag atc tct ttg ata act aac ggg agt tgc ctg 573
Cys Leu Ala Ser Arg Glu Ile Ser Leu Ile Thr Asn Gly Ser Cys Leu
100 105 110

gcc tct gga aag gcc tct ttt atg acg gtc ctg tgc ctt agc agc atc 621
Ala Ser Gly Lys Ala Ser Phe Met Thr Val Leu Cys Leu Ser Ser Ile

EP 2 204 390 A1

115 120 125 130

tat gag gac ttg aag atg tac cag atg gaa ttc aag gcc atg aac gca 669
Tyr Glu Asp Leu Lys Met Tyr Gln Met Glu Phe Lys Ala Met Asn Ala
135 140 145

aag ctt tta atg gat ccc aag agg cag atc ttt ctg gat caa aac atg 717
Lys Leu Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp Gln Asn Met
150 155 160

ctg aca gct atc gat gag ctg tta cag gcc ctg aat ttc aac agt gtg 765
Leu Thr Ala Ile Asp Glu Leu Leu Gln Ala Leu Asn Phe Asn Ser Val
165 170 175

act gtg cca cag aaa tcc tcc ctt gaa gag ccg gat ttt tat aaa act 813
Thr Val Pro Gln Lys Ser Ser Leu Glu Glu Pro Asp Phe Tyr Lys Thr
180 185 190

aaa atc aag ctc tgc ata ctt ctt cat gct ttc aga att cgt gcg gtg 861
Lys Ile Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile Arg Ala Val
195 200 205 210

acc atc gat aga atg atg agt tat ctg aat tct tcc taaaaagctg 907
Thr Ile Asp Arg Met Met Ser Tyr Leu Asn Ser Ser
215 220

aggtctctct cgactttaaa gtcattccta taaaaatgtg aacccaaaag aatttttcat 967

aagatagggg ttaagaacca gggaggggggt ggcttgacct ggtcctactt aagctagtac 1027

gataattctc atgcttgttt acattagttg ccactcaaat tttgaaagat gtgactgtta 1087

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tcgtgagcaa attgctaaag aggaaaaatg tcctcaccga acatgttttt attttccctt 1207

taatagaaga gcaagacttt ataagctatt tctgtaccaa actgtttgta gaaacaaaca 1267

ctcaagcata atttatttaa aaatacttat ttatataatt ttgtgttcat gaaagcatgt 1327

gaattaattt atatttattt atgttatatt tattaaagta tttattatca agtggatttg 1387

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aaaaaaaa 1455

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<212> PRT
<213> Canis familiaris

<400> 105

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20 25 30

Pro Ser Pro Gly Ile Phe Gln Cys Leu Asn His Ser Gln Asn Leu Leu
35 40 45

Arg Ala Val Ser Asn Thr Leu Gln Lys Ala Arg Gln Thr Leu Glu Leu
50 55 60

Tyr Ser Cys Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys Asp
65 70 75 80

Lys Thr Ser Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Thr Met Asn
85 90 95

Glu Ser Cys Leu Ala Ser Arg Glu Ile Ser Leu Ile Thr Asn Gly Ser
100 105 110

Cys Leu Ala Ser Gly Lys Ala Ser Phe Met Thr Val Leu Cys Leu Ser
115 120 125

Ser Ile Tyr Glu Asp Leu Lys Met Tyr Gln Met Glu Phe Lys Ala Met
130 135 140

Asn Ala Lys Leu Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp Gln
145 150 155 160

Asn Met Leu Thr Ala Ile Asp Glu Leu Leu Gln Ala Leu Asn Phe Asn
165 170 175

Ser Val Thr Val Pro Gln Lys Ser Ser Leu Glu Glu Pro Asp Phe Tyr
180 185 190

Lys Thr Lys Ile Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile Arg
195 200 205

Ala Val Thr Ile Asp Arg Met Met Ser Tyr Leu Asn Ser Ser
210 215 220

<210> 106
<211> 1455
<212> DNA
<213> Canis familiaris

<400> 106
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attaattcac atgctttcat gaacacaaaa ttatataaat aagtattttt aaataaatta 180

tgcttgagtg tttgtttcta caaacagttt ggtacagaaa tagcttataa agtcttgctc 240

ttctattaaa gggaaaataa aaacatgttc ggtgaggaca tttttcctct ttagcaattt 300

gctcacgaac acttaactta tccatagtaa atgtgaaata tacttggtca aaggcatcgt 360

gtgggatata acagtcacat ctttcaaaat ttgagtggca actaatgtaa acaagcatga 420

gaattatcgt actagcttaa gtaggaccag gtcaagccac cccctccctg gttcttaacc 480

cctatcttat gaaaaattct tttgggttca catttttata ggaatgactt taaagtcgag 540

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acgaattctg aaagcatgaa gaagtatgca gagcttgatt ttagttttat aaaaatccgg 660

ctcttcaagg gaggatttct gtggcacagt cacactgttg aaattcaggg cctgtaacag 720

ctcatcgata gctgtcagca tgttttgatc cagaaagatc tgcctcttgg gatccattaa 780

aagctttgcg ttcatggcct tgaattccat ctggtacatc ttcaagtcct catagatgct 840

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gcaggcctcc actgtgctgg ttttatcctt tgtgatatct tcatgatcaa tctcttcgga 1020

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gaggaggccg cgcggcgggc acatgctggg cgggcgctgc gtggaccccg gcgggcgctg 1260

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<210> 107
<211> 2267
<212> DNA
<213> Canis familiaris

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<400> 107

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cccagggaac cttgcagcct ggccagaagc aag atg cat cct cag cag ttg gtc      174
                                      Met His Pro Gln Gln Leu Val
                                      1               5

atc tcc tgg ttt tcc ctc gtt ttg ctg gcg tct ccc ctc atg gcc ata      222
Ile Ser Trp Phe Ser Leu Val Leu Leu Ala Ser Pro Leu Met Ala Ile
        10                  15                  20

tgg gaa ctg gag aaa gat gtt tat gtt gta gag ttg gac tgg cac cct      270
Trp Glu Leu Glu Lys Asp Val Tyr Val Val Glu Leu Asp Trp His Pro
    25                  30                  35

gat gcc ccc gga gaa atg gtg gtc ctc acc tgc cat acc cct gaa gaa      318
Asp Ala Pro Gly Glu Met Val Val Leu Thr Cys His Thr Pro Glu Glu
40                  45                  50                  55

gat gac atc act tgg acc tca gcg cag agc agt gaa gtc cta ggt tct      366
Asp Asp Ile Thr Trp Thr Ser Ala Gln Ser Ser Glu Val Leu Gly Ser
                60                  65                  70

ggt aaa act ctg acc atc caa gtc aaa gaa ttt gga gat gct ggc cag      414
Gly Lys Thr Leu Thr Ile Gln Val Lys Glu Phe Gly Asp Ala Gly Gln
            75                  80                  85

tat acc tgc cat aaa gga ggc aag gtt ctg agc cgc tca ctc ctg ttg      462
Tyr Thr Cys His Lys Gly Gly Lys Val Leu Ser Arg Ser Leu Leu Leu
        90                  95                  100

att cac aaa aaa gaa gat gga att tgg tcc act gat atc tta aag gaa      510
Ile His Lys Lys Glu Asp Gly Ile Trp Ser Thr Asp Ile Leu Lys Glu
    105                 110                 115

cag aaa gaa tcc aaa aat aag atc ttt ctg aaa tgt gag gca aag aat      558
Gln Lys Glu Ser Lys Asn Lys Ile Phe Leu Lys Cys Glu Ala Lys Asn
120                 125                 130                 135

tat tct gga cgt ttc aca tgc tgg tgg ctg acg gca atc agt act gat      606
Tyr Ser Gly Arg Phe Thr Cys Trp Trp Leu Thr Ala Ile Ser Thr Asp
                140                 145                 150

ttg aaa ttc agt gtc aaa agt agc aga ggc ttc tct gac ccc caa ggg      654
Leu Lys Phe Ser Val Lys Ser Ser Arg Gly Phe Ser Asp Pro Gln Gly
            155                 160                 165

gtg aca tgt gga gca gtg aca ctt tca gca gag agg gtc aga gtg gac      702
Val Thr Cys Gly Ala Val Thr Leu Ser Ala Glu Arg Val Arg Val Asp
        170                 175                 180

aac agg gat tat aag aag tac aca gtg gag tgt cag gag ggc agt gcc      750
Asn Arg Asp Tyr Lys Lys Tyr Thr Val Glu Cys Gln Glu Gly Ser Ala
    185                 190                 195

tgc ccc tct gcc gag gag agc cta ccc atc gag gtc gtg gtg gat gct      798
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Cys Pro Ser Ala Glu Glu Ser Leu Pro Ile Glu Val Val Val Asp Ala
200                 205                 210                 215

att cac aag ctc aag tat gaa aac tac acc agc agc ttc ttc atc aga      846
Ile His Lys Leu Lys Tyr Glu Asn Tyr Thr Ser Ser Phe Phe Ile Arg
                220                 225                 230

gac atc atc aaa cca gac cca ccc aca aac ctg cag ctg aag cca ttg      894
Asp Ile Ile Lys Pro Asp Pro Pro Thr Asn Leu Gln Leu Lys Pro Leu
            235                 240                 245

aaa aat tct cgg cac gtg gag gtc agc tgg gaa tac ccc gac acc tgg      942
Lys Asn Ser Arg His Val Glu Val Ser Trp Glu Tyr Pro Asp Thr Trp
        250                 255                 260

agc acc cca cat tcc tac ttc tcc ctg aca ttt tgc ata cag gcc cag      990
Ser Thr Pro His Ser Tyr Phe Ser Leu Thr Phe Cys Ile Gln Ala Gln
    265                 270                 275

ggc aag aac aat aga gaa aag aaa gat aga ctc tgc gtg gac aag acc     1038
Gly Lys Asn Asn Arg Glu Lys Lys Asp Arg Leu Cys Val Asp Lys Thr
280                 285                 290                 295

tca gcc aag gtc gtg tgc cac aag gat gcc aag atc cgc gtg caa gcc     1086
Ser Ala Lys Val Val Cys His Lys Asp Ala Lys Ile Arg Val Gln Ala
                300                 305                 310

cga gac cgc tac tat agt tca tcc tgg agc gac tgg gca tct gtg tcc     1134
Arg Asp Arg Tyr Tyr Ser Ser Ser Trp Ser Asp Trp Ala Ser Val Ser
            315                 320                 325

tgc agt taggttccac ccccaggatg aatcttggag ggaaagtgga agatattatg      1190
Cys Ser

caaaattttc taaggacaca ttgaagaggc tccaaaagtt attttctgcc taatttttctt  1250

tttgtaaagg gtcattattg tgtcttcgca atatttttta catttaaatg ccaaatgccc  1310

actgaaacaa tcagctactt tatttataga ttttcagcta gcaggctgcc actgacctta  1370

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tgtgccaaga tatattgtat gtttcatacc ctcaggacct gatctgtaag gaataggccc  1490

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gtgatggatg ggaacacaga ggtagttaaa tagagacatg gagacacgaa tccatttgag  1670

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tttagaaaga cctgagacaa ataactcaaa ttgagattca gcttcagcca ccttgccagt  1850

ccccatcccc atctatctgt aagtcattgg agagtgaccc agggacactg taagtgtctg  1910
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tggtcaagaa ttgcttactg gacagcgcaa gtgaacctga ctggtggatg tgaccagaaa 2090

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<210> 108
<211> 329
<212> PRT
<213> Canis familiaris

<400> 108

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Ala Ser Pro Leu Met Ala Ile Trp Glu Leu Glu Lys Asp Val Tyr Val
20 25 30

Val Glu Leu Asp Trp His Pro Asp Ala Pro Gly Glu Met Val Val Leu
35 40 45

Thr Cys His Thr Pro Glu Glu Asp Asp Ile Thr Trp Thr Ser Ala Gln
50 55 60

Ser Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys
65 70 75 80

Glu Phe Gly Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Lys Val
85 90 95

Leu Ser Arg Ser Leu Leu Leu Ile His Lys Lys Glu Asp Gly Ile Trp
100 105 110

Ser Thr Asp Ile Leu Lys Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe
115 120 125

Leu Lys Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp
130 135 140

Leu Thr Ala Ile Ser Thr Asp Leu Lys Phe Ser Val Lys Ser Ser Arg
145 150 155 160

Gly Phe Ser Asp Pro Gln Gly Val Thr Cys Gly Ala Val Thr Leu Ser
165 170 175

Ala Glu Arg Val Arg Val Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val
180 185 190

Glu Cys Gln Glu Gly Ser Ala Cys Pro Ser Ala Glu Glu Ser Leu Pro
195 200 205

Ile Glu Val Val Val Asp Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr
210 215 220

Thr Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Thr
225 230 235 240

Asn Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg His Val Glu Val Ser
245 250 255

Trp Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu
260 265 270

Thr Phe Cys Ile Gln Ala Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp
275 280 285

Arg Leu Cys Val Asp Lys Thr Ser Ala Lys Val Val Cys His Lys Asp
290 295 300

Ala Lys Ile Arg Val Gln Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp
305 310 315 320

Ser Asp Trp Ala Ser Val Ser Cys Ser
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<210> 109
<211> 2267
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<400> 109
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Date Recue/Date Received 2020-05-26

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